

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2001, 18:10:06 ; Search time 134.89 Seconds  
(without alignments)  
8378.849 Million cell updates/sec

Title: US-09-532-263-4

Perfect score: 1800

Sequence: 1 TCTACACGCTTACCCACT.....TCTTGGAGATTACTACG 1800

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_0601.\*

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21:	/SID88/gcgdata/geneseq/geneseq/NA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1800	100.0	1800	17 AAT17869	Human interleukin-
2	1746.2	97.0	2456	17 AAT33278	Human interleukin-
3	1638.6	91.0	1682	21 AAF20958	Human low adenosin
4	1638.6	91.0	1682	21 AAF21320	Human low adenosin
5	1638.6	91.0	1682	21 AAA34836	Human adenosine re
6	1638.6	91.0	1682	21 AAA35198	Human adenosine re
7	1638.6	91.0	3791	21 AAF20960	Human low adenosin
8	1638.6	91.0	3791	21 AAF21322	Human low adenosin
9	1638.6	91.0	3791	21 AAA34838	Human adenosine re
10	1638.6	91.0	3791	21 AAA35200	Human adenosine re
11	1549.2	86.1	1696	21 AAF20957	Human low adenosin

12	1549.2	86.1	1696	21	AAF21319	Human low adenosin
13	1549.2	86.1	1696	21	AAA34835	Human adenosine re
14	1549.2	86.1	1696	21	AAA35197	Human adenosine re
15	976.4	54.2	1705	17	AAT17868	Murine interleukin
16	954.2	53.0	1714	17	AAT32613	Murine Etl-2 gene.
17	783.6	43.5	1140	21	AAZ40400	Murine soluble int
18	284.2	15.8	296	16	AAT21651	Human gene signatu
19	87	4.8	413	21	AAF20959	Human low adenosin
20	87	4.8	413	21	AAF21321	Human low adenosin
21	87	4.8	413	21	AAA34837	Human adenosine re
22	87	4.8	413	21	AAA35199	Human adenosine re
23	49	2.7	975	21	AAA70701	Human interleukin
24	49	2.7	1035	21	AAZ40288	SR345 coding seque
25	49	2.7	1074	18	AAV04440	Interleukin 6 rece
26	49	2.7	1260	20	AAV09202	Human IL-6 recepto
27	49	2.7	1486	19	AAV60296	Human interleukin-
28	49	2.7	1545	21	AAAT0763	IL-6R/IL-6 fusion
29	49	2.7	1627	18	AAT97848	Human fusion polyp
30	49	2.7	2061	10	AAAN90340	Sequence encoding
31	49	2.7	2066	14	AAQ41746	IL-6 receptor codi
32	49	2.7	2087	10	AAAN90847	DNA contg. region
33	49	2.7	3319	17	AAT31441	Interleukin-6 rece
34	49	2.7	3319	19	AAV60295	Human interleukin-
35	49	2.7	3319	21	AAF21364	Human low adenosin
36	49	2.7	3319	21	AAA35242	Human adenosine re
37	49	2.7	3507	21	AAA09046	Fusion polypeptide
38	49	2.7	4513	21	AAF21365	Human low adenosin
39	49	2.7	4873	21	AAA35243	Human adenosine re
40	47.8	2.7	3477	21	AAA09047	Fusion polypeptide
41	46.2	2.6	1363	19	AAV42919	Truncated Interleu
42	46.2	2.6	1369	19	AAV42918	Truncated Interleu
43	46.2	2.6	2541	12	AAQ13113	DNA encoding IL-6
44	46.2	2.6	2542	13	AAQ24235	IL-6R for soluble
45	44.6	2.5	20674	21	AAQ58017	Arachidonic acid m

#### ALIGNMENTS

RESULT 1

AAT17869

ID AAT17869 standard; DNA; 1800 BP.

AC AAT17869;

XX

XX

DT 21-MAY-1996 (first entry)

XX

DE Human interleukin-11 receptor alpha chain gene.

XX

KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;

KW therapy; diagnosis; ss.

XX

XX Homo sapiens.

XX

XX

XX Key Location/Qualifiers

FT CDS 108..1399

FT /tag= a

FT sig\_peptide 108..196

FT /tag= b

FT mat\_peptide 197..1396

FT /tag= c

XX

XX WO9607737-A1.

XX

XX

PD 14-MAR-1996.

XX

XX

PF 05-SEP-1995; 95WO-AU00378.

XX

XX

PR 05-SEP-1994; 94AU-0007902.

PR

XX

XX 05-SEP-1994; 94AU-0007901.

XX

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX



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RESULT 2
AAT33278
ID AAT33278 standard; cDNA; 2456 BP.
XX
AC AAT33278;
XX
DT 09-OCT-1996 (first entry)
XX
DE Human interleukin-11 receptor cDNA.
XX
KW Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
XX osteoporosis; Paget disease; myeloma; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 734..2002
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
XX
PN W09619574-A1.
XX
PD 27-JUN-1996.
XX
PE 27-NOV-1995; 95WO-US15400.
XX
PR 22-DEC-1994; 94US-0362304.
XX
PA (GEM ) GENETICS INST INC.
XX
PI Tobin JF;
XX
WPI: 1996-309588/31.
P-PSDB; AAR99090.
XX
PT New nucleic acid encoding human interleukin 11 receptor - and
PT related protein, antibodies, receptor antagonists, etc, useful for
PT treating and preventing loss of bone mass
XX
XX Claim 1; Page 31-34; 54pp; English.
XX
CC A cDNA clone (AAT33278) codes for human interleukin-11 (IL-11)
CC receptor (AAR99090), a protein that may play a role in the regulation
CC of bone maturation and repair. The cDNA clone, designated pHLIR14-
CC 2, was isolated from a human activated peripheral blood mononuclear
CC cell cDNA library in ZAPII using probes derived from the murine Etl-
CC 2 gene (see also AAT32613). This sequence, or fragments of it (pref.
CC nts 803-1828, 1907-1999, 734-1999, 1067-1828 or 1067-1999), can be
CC expressed in host systems and the recombinant protein used to treat
CC diseases associated with loss of bone mass or to raise antibodies.
XX
XX Sequence 2456 BP; 487 A; 679 C; 773 G; 517 T; 0 other;
XX
Query Match 97.0%; Score 1746.2; DB 17; Length 2456;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1794; Conservative 0; Mismatches 3; Indels 16; Gaps 3;
QY 1 TCACAGAGCCCTTACCCACTTGTCATCAATTTTCTCTAGGAGCCCTCAGTTTGA 60
DB 606 tcTaaCagccttaccacacttgTgcatacaattttctctctaggaagcctcagtttga 665
QY 61 GAGGAGAGCCAGCCTTTAG-CTCCCATCTCAGGGTCGGGGATTTTGACTCTACTCT 119
DB 666 gadgaagagcaggttttagctccatcctcaggggtcggggtttttgactctacctct 725
QY 120 CCCACAGATGAGCAGAGCTGTGCTGAGGGCTGAGAGGGTCTGCTGGCGCTGGCTACAG 179
DB 726 cccacagatgagcagcagctgtcaggggtcagcaggggtccctgggtggcctggtctacag 785

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QY 180 CCCTGGTGTCTGCTCTCCCTGCCCGCCAGGCTGGGGCCCGCCAGGGGTTCAGTATG 239
DB 786 cctgtgtgtctgctctccctgccccccagcgcctggggccccccaggggtccagtatg 845
QY 240 GGCAGCCAGCAGGTCGTGAAGCTGTGTGCTGCTGAGTGACTGCGGGGAGCCAGTGT 299
DB 846 ggcagccagcaggtcctgtgaagctgtgtgtctgagtgactgcccggggaccagtg 905
QY 300 CCTGGTTTCGGGATGGGAGGCCAAAGCTGCTCCAGGAGACCTGACTCTGGCTAGGGCATG 359
DB 906 cctgggttcctgggagtggggagccaaagctgctccagggacctgactctgggtcagggcatg 965
QY 360 AACTGGTCTCTGGCCAGGAGCAGCAGTGTGATGAGGAGCCTTACATCTGCAGACCCCTGG 419
DB 966 aactggtcctggcccagggcagacagcactgatgaggccactacatctgcagaccctgg 1025
QY 420 ATGGTGCATTTGGGGGACAGTGTGACCTGTGAGCTGGGCTACCTTCCAGCCCGCCTTTG 479
DB 1026 atggtgcacttggggcagcagtgacctgacctgacctgacctgacctgacctgacctg 1085
QY 480 TCTCTGCCAAGCAGCGGACTATGAGAACTTCTTCTGCTTGGAGTCCAGCCAGATCA 539
DB 1086 tctctgccaagcagcagactatgagaactctctctgaccttggagtcctcagccagatca 1145
QY 540 GCGGTTTACCCACCCGCTACCTCCTTACAGGAGAGAGACAGTCTAGGAGCTGATA 599
DB 1146 gcggtttaccacccgctacctcactcctacaggaagacagtcctcagggagctgata 1205
QY 600 GGCAGAGGAGGTTCATCCACAGGGCCCTGGCCATGCCACAGGATCCCTTAGGGGCTG 659
DB 1206 gccagagggaggtccatccacagggcctggcctgacctgacctgacctgacctgacctg 1265
QY 660 CCGCTGTGTGTCTCCAGGGGCTGAGTTCTGAGGCCAGTACCGGATTAATGTACTGAGG 719
DB 1266 ccgctgtgtgtctccacggggtgagttcttggagccagtcctcaggtacaaagtactgag 1325
QY 720 TGAACCCACTGGGTGGTGGCCAGCACAGCCTGCTGGATGTGAGCTTGCAGAGCATCTTGC 779
DB 1326 tgaacccactg---ggtgccagcacacgcctgctggatgtgagcttgcagagcatctgc 1382
QY 780 GCCTTGACCCACCCAGGGGCTGGGGGTAGAGTCAGTACAGGTTACCCCGAGGCCCTGC 839
DB 1383 gccttgaccacccacccagggcctgctgggtagagtcagttaccacaggttaccacccagc 1442
QY 840 GAGCAGCTGCATACCTTGCCTCTGCGCGTGCCAGCCCGCCACTTCTGCTCAAGTTCC 899
DB 1443 gagccagctggagacataccttgcctcctgctgctgctgctgctgctgctgctgctgct 1502
QY 900 GTTTGAGTACCTGTCGGGCGCAGCATCCAGCCTGGTCCAGGGTGGAGCCAGCTGGAGTGG 959
DB 1503 gtttgagtagctccggtccagcagcagcagcagcagcagcagcagcagcagcagcagcag 1562
QY 960 ASGAGGTGATCACAGATGCTGTGGCTGGGCTGGCCCGATGCTGACGAGTACGTCGCCGGG 1019
DB 1563 agsgaggtgatcacagatgctgtggtggtggtggtggtggtggtggtggtggtggtggtg 1622
QY 1020 ACTTTCTAGATGTGGCAGCTTGAGCACCTTGAGGCCCGCGAGGCTGGGAACTCCGAGCA 1079
DB 1623 actttctagatgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1682
QY 1080 CTGGGACCATACCAAGGAGATACACAGATGGGGCCAGCTACACACGACGACGAGGTGG 1139
DB 1683 ctgggaccataccaaagagataccagcatggggccagctacacacgacgacgacgaggtgg 1742
QY 1140 AGCCTCAGGTGGACAGCCCTGCTCTCAAGGCCCTCCCTCCAAACCACACCCCTGGGTAC 1199
DB 1743 agcctcaggtggagagccctgctcctcctcctcctcctcctcctcctcctcctcctcct 1802
QY 1200 TTGATACAGGGACTCTGTGGAGCAGGTAGTGTGCTGGCGTCTTTTGGGAATCTCTTTT 1259
DB 1803 ttgatacaggggactctgttggagcaggtagctgtgtgtgctgtgtgtgtgtgtgtgtgt 1862
QY 1260 TCCTGGGACTGGTGGCTGGGGCCCTGGCTGAGCTGGGGCTCTGGCTGAGCTGAGACGGGGT 1319

```

[illegible]

RESULT	3	
AAF20958		
ID	AAF20958	standard; DNA; 1682 BP.
XX	XX	
XX	AAF20958;	
XX		
DT	14-MAR-2001	(first entry)
XX		
DE	Human low adenosine antisense oligonucleotide related sequence #2525.	
XX		
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;	
KW	human; airway disorder; bronchoconstriction; lung inflammation;	
KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;	
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;	
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;	
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;	
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;	
KW	cancer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200062736-A2.	
XX		
PQ	26-OCT-2000.	
XX		
PF	24-MAR-2000; 2000WO-US08020.	
XX		
PR	06-APR-1999; 99US-0127958.	
XX		
PA	(UYEC-) UNIV EAST CAROLINA.	
PA	(NYCE/) NYCE J W.	

Nyce JW;  
WPI: 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

disclosure; Page 762; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypertensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAR18434 to AAR21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 1682 BP: 324 A: 476 C: 521 G: 361 T: 0 other:

Query Match	91.0%;	Score 1638.6;	DB 21;	Length 1682;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1666;	Conservative 0;	Mismatches 4;	Indels 5;	Gaps 2;
Qy	126	AGATGACGACGAGTGTCTCAGGGCTGACGAGGTCTCTGGTGGCCGTGCTACAGCCCTGG	185	
Db	4	agatgacgacgagctgtccagggtgacgagggctctgtggtggcgtggctacagccctgg	63	
Qy	186	TGTCGTCTCTCCCTCCGCCCCAGGGCTGGGGCCGCCAGGGTCCAGGTATGGGCAGC	245	
Db	64	tgtctgctctccctgtcccccaggcctgggccccccagggtccagtatgggcagc	123	
Qy	246	CAGGAGTCCGTGAAGCTGTGTGTCCTGAGTGACTGCCGGGGACCCAGTGTCTCGT	305	
Db	124	caggcaggtccgtgaagctgtgttctcctggagtgcgtgacggggaccagtgctcctggt	183	
Qy	306	TTCCGGATGGGGACCCAAAGCTGTCCAGGACCTGACTCTGGGCTAGGGATGAACCTGG	365	
Db	184	ttcgggataggggagccaaagctgtcccccaggacctgactctgggctagggcatgaactgg	243	
Qy	366	TCCTGGCCCCAGGCAGACAGCACTGATGAGGCACTACATCTGCCAGACCCCTGGATGGTG	425	
Db	244	tccctggccaggcagacagcactgatgagggcacctacatctgcagaccctggatggtg	303	
Qy	426	CACTTGGGGGCACAGTGAACCTGTGACGTGGGCTACCCCTCCAGCCGCCCTGTGTCTCCT	485	
Db	304	cacttggggcacagtgaacctgcagctgggtgaacctccagccgcgcctgtgtctcct	363	
Qy	486	GCCAAAGCAGCCGACTATGAGAACCTTCTCTGCACTTGGAGTCCCGACCCAGCAGTACACGGTT	545	

Db	1441	tctacctctgatttaccacccagagtgtaggtctctgctcaagaaacggtgtaagtgtac	1500
Qy	1626	ATCTGTGTCCTATGTGTGACCATGTCTGTGAAGCAGGGAACATGTATTCTCTGCATGCA	1685
Db	1501	atctgtgtccatgtgtgacctgtgtctggaagcagggaacatgtattctctgcacgca	1560
Qy	1686	TGTATGTAGTGCCGTGGGAGTGTGTGGGTCCTTGGCTCTTGGCCTTTCCTTTGCACG	1745
Db	1561	tgtatgtaggcgctggggagtggtgtgggtcccttgctctggccttt--ccttgca	1618
Qy	1746	GGGTGTCCAGGTGGAATAAGACAATAAGCAAGCTTCTTGGAGATTATACTCAG	1800
Db	1619	ggggtgtgcaggtgtgaataagagaataaggaagttcttgagattactca	1673
RESULT	4		
AAE21320			
ID	AAF21320	standard; DNA; 1682 BP.	
XX	AC	AAF21320;	
XX	AC		
XX	DT	14-MAR-2001 (first entry)	
XX	DE	Human low adenosine antisense oligonucleotide related sequence #2887.	
KW	KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;	
KW	KW	human; airway disorder; bronchoconstriction; lung inflammation;	
KW	KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;	
KW	KW	immunosuppressive; antiasthmatic;-analgesic; hypotensive; cytotatic;	
KW	KW	respiratory obstruction; pulmonary obstruction; impeded respiration;	
KW	KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	
KW	KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	
KW	KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection	
KW	KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis	
KW	KW	cancer; ss.	
XX	OS	Homo sapiens.	
XX	XX		
XX	PN	WO2000062736-A2.	
XX	XX		
XX	PD	26-OCT-2000.	
XX	XX		
XX	PF	24-MAR-2000; 2000WO-US08020.	
XX	XX		
XX	PR	06-APR-1999; 99US-0127958.	
XX	XX	(UYEC-) UNIV EAST CAROLINA.	
PA	PA	(NYCE/) NYCE J W.	
XX	XX		
XX	PI	Nyce JW;	
XX	PI		
XX	DR	WPI; 2000-679539/66.	
XX	XX		
PT	PT	Low adenosine (A) content antisense oligonucleotides which do not	
PT	PT	trigger adenosine receptors during metabolism, useful e.g. for treating	
PT	PT	cancers and respiratory obstructions -	
XX	XX		
PS	PS	Disclosure; Page 1324-1325; 1592pp; English.	
XX	XX		
CC	CC	The present invention describes low adenosine (A) content antisense	
CC	CC	oligonucleotides and compositions (I) comprising them. In the antisense	
CC	CC	oligonucleotides the A is replaced by a 'Universal' or alternative base;	
CC	CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,	
CC	CC	immunosuppressive, antiasthmatic, hypotensive and cytostatic activities	
CC	CC	The antisense oligonucleotides and (I) can be used to down-regulate the	
CC	CC	expression and or activity of target polypeptides associated with	
CC	CC	lung/respiratory disorders and malignancies, such as stimulating and	
CC	CC	activating peptide factors and transmitters, transcription factors,	
CC	CC	immunoglobulins and antibodies, antibody receptors, cytokines and	
CC	CC	chemokines, endogenously produced specific and non-specific enzymes,	
CC	CC	binding proteins, adhesion molecules and their receptors, cytokine and	
CC	CC	chemokine receptors, adenosine receptors, bradykinin receptors, central	
CC	CC	nervous system (CNS) and peripheral nervous and non-nervous system	

receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impaired respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 1682 BP; 324 A; 476 C; 521 G; 361 T; 0 other;

Query Match 91.0%; Score 1638.6; DB 21; Length 1682;  
Best Local Similarity 99.5%; Pred. NO. 0;  
Matches 1666: Conservative 0; Mismatches 4; Indels 5; Gaps 2;

Qy	126	AGATGACGACGAGCTGCTCAGGGCTGAGCAGGCTCTGTGTGGCCGTGGCTACAGCCCTGG	185
Db	4	agaTgacagcagctgtctcaggctgagcaggtctctgttgccgttggtacagccctgg	63
Qy	186	TGTCGTGCTCTCCCTGCCCCCAGGSCCTGGGGCCCCCAGGGGTCCAGTATGGGCAGC	245
Db	64	tgctgtctctccccctgcccacaggtcttg99gccccca999TcccagtaTg99cagc	123
Qy	246	CAGCAGGTCGTGAAGCTGTGTCTGAGTGACTCCGGGGGACCAGTGTCTCTGGT	305
Db	124	cagcaggtccgtTgaagctgtgttctctgagtgactgc99gggaccagtgctctggt	183
Qy	306	TTCCGGGTGGGGACCAAAAGCTGCTCCAGGGACCTGACTCTGGGCTAGGGCATGAAC	365
Db	184	tctgggtatg99gagcaaaagctgtccaggaagctgactctggcttagggcatgaactgg	243
Qy	366	TCCTGGCCAGGACAGACAGACACTGATGAGGGCACCTACATCTGCCAGACCTCGGATGGTG	425
Db	244	tcctTgcccaggcagacagcaactTgaTgagggcaactacatctgcacagacctTggtTgTg	303
Qy	426	CACTTGGGGGCACAGTGACCCCTGCAGCTGGGCTACCCCTCAGCCGCCCTGTGTGCTCTCT	485
Db	304	caactTgggggcaagtgacactgcagctgggtcacctccagccgcgacctgtgtctctct	363
Qy	486	GCCAAGCAGCGCACTATGAGAACTTCTTTGCACTTGGAGTCCAGCCACAGATCAGCGGTT	545
Db	364	gccaagcagccgactaTgaagactctctTgcaactTg99agctccagTccagTccagc99ct	423
Qy	546	TACCCACCCGCTACCTCACCTCTACAGGAAGACAGTCTCTAGAGCTGATGCCAGA	605
Db	424	TaaccacccgtactcactcactcactacaggaagacagTccttagTgctgatagcaga	483
Qy	606	GGAGGATCCATCCACAGGGCCCTGGCCATGCCACAGGATCCCCTAGGGGCTGCCGCT	665
Db	484	ggaggtTccatccacagggccctTgccaTgcccacagatccctcaggggtgcccct	543
Qy	666	GTGTGTGCCAGGGGCTGAGTCTTGAGGACAGTACCGGATTAATGTCACTGAGGTGAACC	725
Db	544	gtgtTgccacgggctTgagtTctggaGCCagTaccggtattatTgactgaggtgaacc	603
Qy	726	CACTTGGGTGTGCCAGCACAGCCCTGCTGGATGTGAGCTTGCAGACGATCTTGGCCGCTG	785
Db	604	cactgT---ggTgcagcacacgctgtctggtatTgagctTgcagatctTgcgcctg	660
Qy	786	ACCCACCCACGGGCTCGGGGTAGAGTCACTACAGGTTACCCGCCAGGCTCGCAGGCCA	845
Db	661	accacccccaggccctg99gtagTccagTccaggtTaccccccagccctTgcagcca	720
Qy	846	GCTGGACATACCTTGCTCTCTGGCCGTGCCAGGCCCACTCTGTCTCAAGTTCCTGTTTC	905



KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 \*XX Homo sapiens.  
 XX WO200009525-A2.  
 PN 24-FEB-2000.  
 XX 03-AUG-1999; 99WO-US17712.  
 XX 03-AUG-1998; 98US-0095212.  
 PR (UYEC-) UNIV EAST CAROLINA.  
 PA NYce JW;  
 XX WPI; 2000-205971/18.  
 DR New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers -  
 XX Disclosure; Page 691-692; 1343pp; English.  
 XX The present invention describes a new composition comprising an  
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytotatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of  
 CC the ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
 CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
 CC invention. N.B. Sequences given in the disclosure of the present  
 CC invention do not match up with their corresponding SEQ ID NO: sequences  
 CC given in the sequence listing.  
 XX  
 XX Sequence 1682 BP; 324 A; 476 C; 521 G; 361 T; 0 other;  
 SQ

Query Match 91.0%; Score 1638.6; DB 21; Length 1682;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1666; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

QY 126 AGATGACAGAGCTGCTCAGGGCTGACAGGGGTCCTGGCGCTGACAGCCCTGG 185  
 DB 126 AGATGACAGAGCTGCTCAGGGCTGACAGGGGTCCTGGCGCTGACAGCCCTGG 185  
 QY 186 TGTCTGCTCTCTCCCTGCCCCAGGCTGGGCCCCCCCCAGGGGTCAGTATGGGAGC 245  
 DB 64 TGTCTGCTCTCTCCCTGCCCCAGGCTGGGCCCCCCCCAGGGGTCAGTATGGGAGC 123

QY 246 CAGCAGGTCCTGCTGAAAGCTGTGTGCTCTGAGTACTGCCGGGACCCAGTGTCTCTGGT 305  
 DB 124 caggcaggtccgtgaagctgtgttctctgagtgactgctgcggggaccacagtgctctggt 183  
 QY 306 TTCCGGATGGGGAGCCAAAGCTGCTCCAGGAGCTGACCTCTGGCTAGGCGATCAACTGG 365  
 DB 184 ttcgggatggggagccaaagctgctccaggagactgactctggctgagggcagtggaactgg 243  
 QY 366 TCTGTGCCCCAGGACAGACACTGATGAGGGCACCTACATCTGCCAGACCCCTGATGGTG 425  
 DB 244 tctgtgcccaaggacagacagcactgatgagggcaacctacatctgccagaccctgagtggtg 303  
 QY 426 CACTTGGGGCACAGTACACCTGCAGCTGGGCTACCCCTCCAGCCCGCCCTGTGTCTCTCT 485  
 DB 304 cacttggggcacagtgacccctgagctgggtacccctccagcccgccctgtgtctctct 363  
 QY 486 GCCAAGCAGCCGACTATGAGAACTTCTTTCACCTTGGAGTGGAGTCCAGCCAGATCAGCGGTT 545  
 DB 364 gccaaagcagccgactatgagaacttctcttgacactggagctccagccagcagatcagcggtt 423  
 QY 546 TACCACACCCGCTACCTCACCTCCTACAGGAAGAACAGTACCTAGGAGCTGATAGCCAGA 605  
 DB 424 taccacccgctacctcaacctctacaggaagaagacagtcctagagagctgatagccaga 483  
 QY 606 GGAGGAGTCCATCCACAGGCCCCCTGGCCATGCCCCACAGGATCCCTTAGGGGCTGCCCGCT 665  
 DB 484 ggagagtgccatccacagggccctggcctgacacagagatccctctaggggctgcccgt 543  
 QY 666 GTGTTGTCACGGGGCTGAGTCTTGAGAGCCAGTACCCGGATTATGTGACTGAGGTGAACC 725  
 DB 544 gtgtgtccacggggctgagttcttgagccagtagccgagattatgtgactgaggtgaacc 603  
 QY 726 CACTTGGTGTGTCAGCACACGCTGCTGGATGTGAGCTTGCAGAGCATCTTTCGCCCTG 785  
 DB 604 cactg---ggctccagcacacgctgctggatgtgagcttgagagacatctgcgcctg 660  
 QY 786 ACCACCCCCAGGGCTCGGGGTAGAGTACAGTACAGGTTACCCCGAGGCTCGGAGCCA 845  
 DB 661 accaccccgagggcctgcgggtagatcagtagtaccaggtaccaccccgacgctgcgagcca 720  
 QY 846 GTGAGACATACCTGCTCTCTGGCGTGGCCAGCCACCTTCTGCTCAAGTTCGGTTGC 905  
 DB 721 gctggacataacctgctcctctgctgctggcagcccaactctctgctcaagtctcgtttgc 780  
 QY 906 AGTACGCTCCGGCGCAGCATCCAGCCCTGCTCCAGGGTGGAGCCAGCTGGAGGAGG 965  
 DB 781 agtaccgtccggcgagcatccagccttgcctccagcgggagcagctggagctggaggg 840  
 QY 966 TGATCAGAGATGCTGTGGCTGGGCTGCCCTATGCTGTACAGTACAGTCCCGGAGCTTC 1025  
 DB 841 tgatcacagatgctgtgctggctgccccatgctgtacagtcagtgccccggacttc 900  
 QY 1026 TAGATGTGACCTGAGGACCTGAGACCCGGAGGCTGGGAACTCCGAGGACTGGGA 1085  
 DB 901 tagatgtgcacgtgagcacctggagcccgaggctggggaactccagagcactggga 960  
 QY 1086 CCATACCAAGAGAGATACAGCATGGGGCCAGCTACACAGCAGCCAGAGGTGGAGGCTC 1145  
 DB 961 ccataccaaaggagataccagcagctcggggcagctacacagcagcagagagtgagcctc 1020  
 QY 1146 AGGTGGAGACCCCTGCTCTCCAGAGGCCCTCCCTCCAAACACACCCCTCGGCTACTGTATC 1205  
 DB 1021 aggtggacagccctgctctccaaaggccctccctcccaacacacacccctcggtactgtatc 1080  
 QY 1206 ACAGGGACTCTGTGGACAGGTAGCTGTGCTGGCGCTCTTTGGGGAATCCTTCTTCTG 1265  
 DB 1081 acagggactctgtgagcagcagtagctgtgctgctgtttggggaatcctcttctctctg 1140  
 QY 1266 GACTGTGGCTGGGGCCCTGGCACTGGGGCTCTGGCTGAGGCTGAGAGCGGGGTGGGAGG 1325  
 DB 1141 gactgtgtgctggggccctggcagctggggcctggcctgagctgagagcgggggtggaggg 1200  
 QY 1326 ATGGATCCCCAAAGCCCTGGGTTCTTTGGCCCTCAGTGTATTCAGTGACAGGCGTCCAGGAG 1385

Db 1201 atggatcccaagagctgggtcttggctcagtgattccagtgacagggctccaggag 1260  
Qy 1386 CTCCTAAACCTGTAGAGGACCCAGGAGGCTTCGGCAGATTCCACCTATAATCTCTCTTG 1445  
Db 1261 ctccaaacctgtagaggacccaggggcttcggcagatccaccataaattctgtcttg 1320  
Qy 1446 CTGGTGTGATAGAAACAGGACGACAGTAGATCCCTATGTTGGTTCATCTCAGCTGGAAG 1505  
Db 1321 ctgggtgtgataaaccagcagcagcagcagcagcagcagcagcagcagcagcagcag 1380  
Qy 1506 TTCTGTGGACCCCATTTCTGTGACACCTGTATTTCAAATTCACGCTGAAGAGTGCT 1565  
Db 1381 tctctttggagccattctgtgagaccctgtatttcaaatgttcagctgaaagtgtct 1440  
Qy 1566 TGTACTCTGTATTTCACCCACAGTTGGAGTCTCTCAAGGAAGCTGTGTAATGTGTAC 1625  
Db 1441 tctactctgtatttcaacccagagtggtggtcttctcgaaggagcgtgtgtaagtgtac 1500  
Qy 1626 ATCTGTGTCATGTGTGACCATGTCTGTGTGAAGCAGGGAACATGATTTCTGTGATGCA 1685  
Db 1501 atctgttccatgtgtgacatgtctgtgagcagcagcagcagcagcagcagcagcagc 1560  
Qy 1686 TGTATGTAGTCCCTGGGAGTGTCTGTGGTCTTGGCTTGGCTTGGCTTGGCTTGGCT 1745  
Db 1561 tgtatgtaggtgctcgggagtggtgtggttccctgtgctcttggccttt--ccttgag 1618  
Qy 1746 GGGTGTGTCAGGTGTAATAAGAGAATAAGGAAGTCTTGGAGATTATCTACG 1800  
Db 1619 ggggtgtgcaggtgtgaataaagaagaataaaggaaagttcttggagattactcag 1673

RESULT 6  
AAA35198  
ID AAA35198 standard; DNA; 1682 BP.  
XX  
AC AAA35198;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:72.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytotostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US17712.  
XX  
PR 03-AUG-1998; 98US-0095212.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers  
XX  
PS Disclosure; Page 1241; 1343pp; English.

XX The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, cystic  
CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of  
CC the ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
CC invention. N.B. Sequences given in the disclosure of the present  
CC invention do not match up with their corresponding SEQ ID NO: sequences  
XX given in the sequence listing.  
SQ Sequence 1682 BP; 324 A; 476 C; 521 G; 361 T; 0 other;

Query Match 91.0%; Score 1638.6; DB 21; Length 1682;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1666; Conservative 0; Mismatches 4; Indels 5; Gaps 2;  
Qy 126 AGATGAGCAGCAGCTGCTCAGGCGCTGACAGGGTCTTGGTGGCGCTGCTACAGCCCTGG 185  
Db 4 agatgagcagcagctgctcagggctgagcagggctgctggtgctgagcagccctgg 63  
Qy 186 TGTGTGCTCTCCCTCCCTGCGCCCGCCAGGCGCTGGGGCCCCCAGGGGTCCAGTATGGCAGC 245  
Db 64 tgtctgctctccctctgccccagggcctggggccccccaggggtccagtatggcagc 123  
Qy 246 CAGCAGCTGCTGCTGAAGCTGTGTCTGTGAGTACTGTCGGGGAGCCAGTGTCTCTGCT 305  
Db 124 cagcagctgctgtaagctgtgtctctgagtgactgctgctgctgctgctgctgctgct 183  
Qy 306 TTCGGGATGGGAGCCAAAGCTGCTCCAGGACCTGACTCTGGGCTAGGGATGAACCTGG 365  
Db 184 ttcg99gatggggccaaagctgctccagggacctgactctg99gctg99gcatgaactcgg 243  
Qy 366 TCCTGGCCCGCAGCAGCAGCAGCTGATGAGGCGACCTACATCTGCCAGACCCCTGGATGGTG 425  
Db 244 tcttggcccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 303  
Qy 426 CACTTGGGGGACAGTACCTGACCTGAGTGGGCTACCCCTCCAGCCGCGCTGTGTCTCT 485  
Db 304 cacttgggggacagtgacctgacctgacctgacctgacctgacctgacctgacctgacct 363  
Qy 486 GCCAAGCAGCGCAGTATGAGAACTCTTGTGACTTGGAGTCCCGAGCCAGATCAGCGGTT 545  
Db 364 gccaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 423  
Qy 546 TACCCACCCGCTACCTCACCTCTACAGGAAGACAGTCTCTAGGAGCTGATAGCCAGA 605  
Db 424 taccaccccgctacctacctacctacctacctacctacctacctacctacctacctacct 483  
Qy 606 GGAGAGTCTCATCCACAGGGCCCTGGCCATGCCACAGAGTCCCTAGGGGCTGCCCTCT 665  
Db 484 ggaggagtcctacacagggccctggccatgccacaggaatccccctaggggctgcccct 543  
Qy 666 GTGTGTGTCAGGGGCTGAGTTCGGAGCCAGTACCCGAGTAAATGTGACTGAGGTGAACC 725  
Db 544 gtgtgtccacggggtgagttcttggagccagtagtccagcagcagcagcagcagcagcagc 603



RESULT	7
AAAF20960	
ID	AAAF20960 standard; DNA; 3791 BP.
XX	
AC	AAAF20960;
XX	
DT	14-MAR-2001 (first entry)
XX	
DE	Human low adenosine antisense oligonucleotide related sequence #527.
XX	
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
human; airway disorder; bronchoconstriction; lung inflammation;	
KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW	cancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200062736-A2.
XX	
PD	26-OCT-2000.
XX	
PF	24-MAR-2000; 2000WO-US08020.
XX	
PR	06-APR-1999; 99US-0127958.
XX	
PA	(UYEC-) UNIV EAST CAROLINA.
PA	(NYCE/) NYCE J W.
XX	
PI	Nyce JW;
XX	
DR	WPT; 2000-679539/66..
XX	
PT	Low adenosine (A) content antisense oligonucleotides which do not
PT	trigger adenosine receptors during metabolism, useful e.g. for treating
PT	cancers and respiratory obstructions .
XX	
PS	Disclosure; Page 763-764; 1592pp; English.
XX	
CC	The present invention describes low adenosine (A) content antisense
CC	oligonucleotides and compositions (I) comprising them. In the antisense
CC	oligonucleotides the A is replaced by a 'Universal' or alternative base
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC	immunosuppressive, antiasthmatic, hypotensive and cytostatic activities
CC	The antisense oligonucleotides and (I) can be used to down-regulate the
CC	expression and or activity of target polypeptides associated with
CC	lung/respiratory disorders and malignancies, such as stimulating and
CC	activating peptide factors and transmitters, transcription factors,
CC	immunoglobulins and antibodies, antibody receptors, cytokines and
CC	chemokines, endogenously produced specific and non-specific enzymes,
CC	binding proteins, adhesion molecules and their receptors, cytokine and
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central
CC	nervous system (CNS) and peripheral nervous and non-nervous system
CC	receptors, CNS and peripheral nervous and non-nervous system peptide
CC	transmitters, defensins, growth factors, vasoactive peptides and
CC	receptors, binding proteins and malignancy associated proteins. The
CC	antisense oligonucleotides may be used in this way to treat disorders
CC	including respiratory obstruction (especially pulmonary obstruction
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC	and/or surfactant hypoproduction which are associated with a disease or
CC	condition selected from pulmonary vasoconstriction, inflammation,
CC	allergies, asthma, impeded respiration, respiratory distress syndrome
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC	fragments and antisense oligonucleotides used in the exemplification of







Qy	846	GCTGGACATACCCTGCTCCTTGCGCGTGCAGCCGCCACTTCCTGCTCAAGTTTCGGTTTGC	905
Db	2417	gctggacataccctgctcctgctgcgtgccagccccacttctgctcaagtctcggttc	2476
Qy	906	AGTACGCTCGGGCGCAGCATCAGACTGGTCCACGGTGGACCCAGCTGGACTGGAGGAGG	965
Db	2477	agtacgctcggcgagcatccagcctggtccaoggtggagcccagctcggaactggaggaagg	2536
Qy	966	TGATCACAGATGTGTGGCTGGGCTGCCCATCTGTGTACGAGTCAGTCCCGGACATTTC	1025
Db	2537	tgatcacagatgctgtgctggctggcctggcccatgctgtacagtgcafgccccggaccttc	2596
Qy	1026	TAGATGCTGGCACCCTGGACACCTCGAGCCCGAGGCCCTGGGAACCTCCGAGACCTGGGA	1085
Db	2597	tagatgctggcaccctggacacctggagcccgagcctggggaaactccgagcacatggga	2656
Qy	1086	CCATACCAAAGGAGATACCAGCATGGCGCCAGCTACACACGCCAGCCAGAGGTGGAGCCTC	1145
Db	2657	ccataccaaaggaga taccagcatggggccagctaca cagcagcagagtgtagagcctc	2716
Qy	1146	AGGTGACAGCCCTGCTCCTCCAAGGCCCTCCTCCAAACCACCCCTCGGCTACTTCGATC	1205
Db	2717	aggtggacagccctgctcctccaaggccctcccaaccacacccctcgctacttgatc	2776
Qy	1206	ACAGGACTCTGTGGAGCAGTAGCTGTGCTGGCGCTTTTGGGAATCCTTTCTTCTCTGG	1265
Db	2777	acaggacctctgtgagcaggtagctgtgtgtggctctttgggaatcctcttcttcctgg	2836
Qy	1266	GACTGTGGCTGGGGCCCTGGCACTGGGGCTCTGGCTGAGGCTGAGACGGGGTGGGAAGG	1325
Db	2837	gactgtggctggggccctggcactgggctctggctgagctgagacggggtgggaagg	2896
Qy	1326	ATGGATCCCCAAGCCTGGTCTTTGGCCTCAGTGATTCACAGTGGACAGCGCTCCAGGAG	1385
Db	2897	atgga tccccaagcctgggtctctggcctcagtgatcccaagtggacagcgctccaggag	2956
Qy	1386	CTCCAACCTGTAGAGACCCAGGAGGCTTCGGCAGATTCCACCTATAATCTGCTCTTG	1445
Db	2957	ctccaaactgtaggaccagcagggtctcgagattccacctataattctgtcttg	3016
Qy	1446	CTGGTGTGGATAGAACACGAGGACAGTAGATCCCTATGTTGGATCTCAGCTGGAG	1505
Db	3017	ctggtgtgatatgaaccaggcaggacagttagatccctatggttggatctcagctggagg	3076
Qy	1506	TTCTGTTTGGAGCCCATTCTGTGAGACCCGTATTTCAAATTTGCAGCTGAAAGTGCT	1565
Db	3077	tctgttgttgagcccaattctgtgagacccgttatctcaaatttgcagctgaaaagtgc	3136
Qy	1566	TGTACCTCTGATTTCACCCAGAGTTGGAGTTCTGCTCAAGSACAGTGTGTAATGTGTAC	1625
Db	3137	tctacctctgattctaccccagagtgtgagttctgtctcgaaggaaagtgttaa lgtgtac	3196
Qy	1626	ATCTGTCTCATGTGTGACCATGTCTGTGAAGCAGGGAACATGTATTCTCTCATGTCA	1685
Db	3197	.atctgttccatgtgtgaccatgtctgtgagcgaggaaacatgtattctctgcatgca	3256
Qy	1686	TGATGTAGTGCCTGGGAGTGTGTGGGTCCCTTGGCCTTTGCCCTTTGCCCTTGCAG	1745
Db	3257	tgtatgtaggctgctgggagtggtgtgtgggtcccttgctcttgccctt--cctgcag	3314
Qy	1746	GGGTGTGCAGGTGTGAATAAGAGAANAAGGAAGTCTTTCGGAGATTATACTCAG	1800
Db	3315	gggtgtgcaggtgtgaa laagagaataaaggaagctcttgagatatactcaq	3369

RESULT 10  
AAA35200  
ID AAA35200 standard; DNA; 3791 BP  
XX  
XX AAA35200;  
XX  
DT 28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide 2nd SEQ ID NO:74.

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPT: 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers -

Disclosure; Page 1241-1242; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 3791 BP: 716 A: 1087 C: 1151 G: 837 T: 0 other:

	Query Match	91.0%	Score 1638.6	DB 21	Length 3791	
	Best Local Similarity	99.5%	Pred. No. 0			
	Matches 1666	Conservative 0	Mismatches 4	Indels 5	Gaps 2	
QY	136	AGATGACGAGCAGCTGCTCAGGGCTTGACAGGGTCTCTGGTGGCCCTGCTACAGCCCTGG	185			
DB	1700	agatgagcagcagctgctcagggtgagcagggtcctggtgcccgtggtctacagccctgg	1759			
OV	186	TGTCGTGCTCTCTCCCTGCCCCCAGGGCTGGGGCCCCCCCCAGGGGTTCAGTATGGGCAGC	245			





Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -  
 Disclosure; Page 761-762; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 1696 BP; 315 A; 488 C; 529 G; 364 T; 0 other;

Query Match 86.1%; Score 1549.2; DB 21; Length 1696;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 1621; Conservative 0; Mismatches 18; Indels 11; Gaps 5;

121 CCCACAGATGAGCAGAGTCTCAGGGCTGAGCAGGGTCTCTGGTGGCGTGGCTACAGC 180  
 55 caccagatgagcagcagctgctcaggctgagcaggtccctggtggcgtggtcctacac 114  
 181 CTGTGTCTGCTCTCCCTGCTCCCGCAGCCTGGGGCCCGCCAGGGGTCCAGTATGG 240  
 115 cctggtgtgctcctcctccctgccccagcctggggccccccaggggtccagtatg 174  
 241 GCAGCCAGCAGGTCGCTGAAGCTGTGTGCTCTGGAGTACTGCGGGGACCCAGTGTC 300  
 175 gcagccagggaggtccgfgaagctgtgtcctctggagtgactgctcggggagccagtg 234  
 301 CTGGTTCCGGGATGGGAGCCAAAGCTGCTCCAGGACCTGACTCTGGGCTAGGCGATCA 360  
 235 ctggtttcggatgggagccaaagctgctccagggacctgactctggcgtaggcatga 294  
 361 ACTGTCTCGGCCAGGAGACAGCAGCTGATGAGGACCTTACATCTGCCAGACCTTGA 420  
 295 actggtctctggccagggagacagcactgatgagggcactcatctgcagacccttga 354  
 421 TGGTGACATTTGGGGCACAGTACCTCGAGCTGGGCTACCTCCAGCCCGCCCTGTCTG 480  
 355 tgggtgactctggggcagcagtgacctgagctgggctacctccagcccgccctgtgt 414  
 481 CTCCTGCCAAGCAGCGGCTATGAGAACTCTCTTGGCACTTGGAGTCCCGAGCCAGATCAG 540  
 415 ctccctgccaagcagccgactatgagaactctctgcacttgagtgccagccagatcag 474  
 541 CGGTTTACCCACCGCTACCTCCTCTACAGGAAGAACAGCTCCTTAGGAGCTGATAG 600

475 cggttattccccccgctactcactcctctacaggaagaagacagtcctctagagctgatag 534  
 601 CCAGAGGAGGAGTCCATCCACAGGGCCCTGGCCATGCCACACAGGATCCCTTAGGGCTGC 660  
 535 ccagaggaggagtgccatccacagggcccttgccatgccccacaggaatccccctagggtgc 594  
 661 CGCTGTGTGTTCACCGGGCTGAGTTCCTGGAGCCAGTACCAGATTAATGTGACTGAGT 720  
 595 cgcgtgtgtgtccacgggctgagttcttgagccagtagtaccgatttaattgactgaggt 654  
 721 GAACCCACTGGGTGGTGGCCAGCACAGCCCTGCTGGATGTGAGCTTCACAGACATCTTGG 780  
 655 gaaccactg---gggtgccagcacgcctgctggtgagcttgagcttgacagacatcttgc 711  
 781 CCCTGACCCACCCAGGGCTCGGGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 840  
 712 ccttgacccacccagggcctgctgggtagtagtaccaggttaccacccagcagcctgcg 771  
 841 AGCCAGCTGGACATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 772 agccagctggacataccctgctcctcctgctgctgctgctgctgctgctgctgctgctg 831  
 901 TTTGAGTACCTGCTGGCGCAGCATCCAGCTGGTCCAGCTGGAGCCAGCTGGAGCTGGA 960  
 832 ttgtcagtagctgctggcgagcagcctcagcctggtccacggtggagccagctggactgga 891  
 961 GGAGTGTATCAGAGTGTGTGGTGGCTGCCCATGCTGTACGAGTACGAGTACGAGTACG 1020  
 892 ggaagtgtgacacagatgctgtgctgggctggcccatgctgtacagagtcagtgcccgga 951  
 1021 CTTTCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 952 cttcttagatgctggcaccctggagcaccctggagcccgagcctggggaacccagagcac 1011  
 1081 TGGGACCATACCAAGGAGATACAGCATGGGGCCAGCTACACACCCAGCCAGAGGTGGA 1140  
 1012 tgggacctatcccaaggagataccagatggggccagctacacacagcagccagaggtgga 1071  
 1141 GCCTAGGTGGAGACGCCCTGCTCCCAAGGCCCTCCCAACACACACCCCTGGGCTACT 1200  
 1072 gctcagggggagacagcctgctcctccaaaggccctccctcccaacacacccctggctact 1131  
 1201 TGATCACAGGGGACTCTGTGGAGCAGTACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 1132 tgatcacagggactctgtgagcagtagctgtgctgctgctgctgctgctgctgctgctt 1191  
 1261 CTGGGACTGTGTGGTGGGGCCCTGGCAGCTGGGGCTGCTGGCTGAGCTGAGACGGGGTGG 1320  
 1192 cctggagctggtggctggggccctggcactgggctgctgctgctgctgctgctgctgctg 1251  
 1321 GAAGGATGATCCCAAGGCCCTGGGTTCTTGGCTCAGTATTCCAGTGGACAGCGGTCC 1380  
 1252 gaagtgatgagatcccccaaacctgggtctctggcctcagtgattccagtgagcagggctcc 1311  
 1381 AGGAGCTCCAAACCTGTAGAGGACCCAGAGGGCTTTCGGCAGATTCCACTATAATCTCTG 1440  
 1312 aggaagctccaaacctgtagaggaccagagggcttcgagagattccacctataattctg 1371  
 1441 TCTTCTGTGTGTGGATAGAAACCCAGCAGCAGATAGATCCCTATGTTGGATCTCAGCT 1500  
 1372 tcttctgctggtggtatagaacacagcagtagatccctctggttggatctcagct 1431  
 1501 GGAAGTCTGTTTGGAGCCCATTTCTGTGAGACCCCTGTATTTCAAAATTTGCAGCTCAAG 1560  
 1432 ggaagttctgttggagcccatctctgtgagaccctgtatttcaaatattgagcagtgaaag 1491  
 1561 GTGCTGTGACCTCTGATTTACCCAGAGTGTGGAGTCTGCTCAAGGAACAGTGTGTAATG 1620  
 1492 gfgctgtgtacctctgatttcccccagagttgaggtctctgctcaaggaacggtgtgaaag 1551  
 1621 TGTACATCTGTCTCCATGTGTGACCATGTGTCTGTGGAAG--CAGGGAACATGTATT-CTC 1677  
 1552 tgtacatctgtgtccatgtgtgacctgtgtctgtgagggccaggaacatgtattcctc 1611



QY	961	GGAGGTGATCACAGATGCTGTGGCTGGCGTCCCCCATGCTGTACGAGTCACTGCCCGGGA	1020
Db	9892	ggagggtgatacaagatgctgtgtgctggcgtgcccctgctgtaagatcagtgcccggga	951
QY	1021	CTTCTTAGATGTGGCACCTCGAGCACCTGGAGCCGAGGCGCTGGGGAACCTCCGAGCAC	1080
Db	952	ctttetagtgtgcaactgagacactgagccggagcgttgggaaactccgagcac	1011
QY	1081	TGGGACCATACMAAGAGATACCAAGATGAGGCGCAGCTACACACGACGACGAGGTGGA	1140
Db	1012	tgggacataaccaagagatataccagcatggggcagctacacacgagccagaggttggga	1071
QY	1141	GCCTCAGGTGGACAGCCCTGCTCTCAAGGCGCTCCCTCAACACACACCTCGGCTACT	1200
Db	1072	gcctcagggtggacagccctgtctctccaaaggccctccctcaacacacacctggctact	1131
QY	1201	TGATCACAGGGACTCTGTGGACAGGTAGCTGTGCTGGCGCTCTTTGGGAATCCTTCTTT	1260
Db	1132	tgatcacaggacctgtgtgagcaggtagctgtgtgctgtctttgggaaactccttcttt	1191
QY	1261	CTTGGGACTGTTGGCTGGGGCCCTGGCACTGGGCTCTGGGCTGAGGCTGAGACGGGTGG	1320
Db	1192	ctctgggactgtgtgtgtggggccctggcactgggctctgtgtgagctggagcgggtgtg	1251
QY	1321	GAAGGATGGATCCCAAGACCTTGGGCTTCTGGCTCAGTGATTCCAGTGGACAGGCGTCC	1380
Db	1252	gaaggatgatatcccaaaagcctggcttctgtgctcagtgattccagtggaacggctcc	1311
QY	1381	AGAGCTCCMAACCTGTAGAGGACCCAGAGGGCTTGGCGAGATTCACCTATAATCCTG	1440
Db	1312	agagctccaaacctgtadagagccacagagggtctggcgagattccacctataactctg	1371
QY	1441	TCCTTGCTGTGTGGATAGAAACAGCGAGGACAGTAGATCCCTATGTTGGATCTCAAGT	1500
Db	1372	tcttgcgtgtgtgatagaaaacacagagacagtagatccctatggttgagatccagct	1431
QY	1501	GGAGTTCGTTTGGAGCCCATTTCTGTGAGACCTCTGATTTCAAAATTTGCAGCTGAAG	1560
Db	1432	ggaagttctgtttggagccatttctgtgagaccctgtatttcaaaatttgcagctgaaag	1491
QY	1561	GTGCTGTACTCTGTATTTACCCACAGAGTTGGAGTTCCTGCTCAAGAAAGTGTTAATG	1620
Db	1492	gtccttgtacctctgatttcaacccagagtttggagttctgtctcaaggaaacgtgttaagt	1551
QY	1621	TGTACATCTGTGTCCATGTGTGACCATGTGTCGTGTGAAG--CAGGAAACATGTATT--CTC	1677
Db	1552	tgtacatctgtgtccatgtgtgaccatgtgtctgttgaaggccagggaacatgtattctctc	1611
QY	1678	TGATGCACTATGTAGGTGCGCTGGGGAGTGTGTGGGCTCTTGGCTCTTGGCTTTTC	1737
Db	1612	tgatgcatactatgttaagggtcctgtg---gagtggtgtgtgtctctgtctgtggcccttccc	1668
QY	1738	CTTGCAGGGGTTGTCCAGGTGTGAATAAA	1767
Db	1669	c---ttacagagtttgcagatgtgaataaa	1696

RESULT 13

RESOL  
AAA34835

AAA34833  
ID AAA34835 standard: DNA: 1696 bp

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AC YY AAAA.

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28-III-2000 (first entry)DT 28-0  
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KW Human

respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
cancer; leukemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary  
vasoconstriction, inflammation, allergies, asthma, hypertension, or  
bronchitis, emphysema, respiratory distress syndrome, ischemia or  
cancers -

Disclosure; Page 691; 1343pp; English.

The present invention describes a new composition comprising an  
antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
targets nucleic acids involved in bronchoconstriction, allergies, and/or  
inflammation. The ON can have antiinflammatory, antiallergic,  
antiasthmatic, cytostatic and analgesic activities. The compositions are  
useful for the treatment of diseases associated with inflammation,  
impaired airways, including lung disease and diseases whose secondary  
effects afflict the lungs of a subject. They can be used for treating  
e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
carcinomas, and cancers which may metastasize to the lungs, including  
breast and prostate cancer. The reduction of the adenosine content of  
the ONs reduces side effects. The A-containing ONs break down with the  
release of deoxyadenosine which activates adenosine receptors causing the  
bronchoconstriction and inflammation. AAA32313 to AAA3312 represent the  
nucleotide sequences given in the sequence listing from the present  
invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
differ from the previously named sequences. SEQ ID NO:11 to 1680  
(AAA32323 to AAA33992) are specifically claimed ONs from the present  
invention. N.B. Sequences given in the disclosure of the present  
invention do not match up with their corresponding SEQ ID NO: sequences  
given in the sequence listing.

Query Match 86.1%; Score 1549.2; DB 21; Length 1696;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 18; Indels 11; Gaps 5;

121 CCCACAGATGAGCAGCAGCTGCTCAGGGCTGAGCAGGGTCCCTGGTGGCCGTGGCTACAGC 180

7 121 CCCAÇAGATAGCAGCAGCAGCAGGCTCAGGCTGAGCAGGCTCCAGGCTACAGC 180

55 caccgaatgaacagcagcagctgctcagggctgaacagggctcctggtgcccgtggtacagc 114

[illegible]

181 CCTGGTGTCTGCCCTCCTCCCCCTGCCCCAGGCCCTGGGGCCCCCAGGGTCCAGTATGG 240

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115 cctggtgtgtgcctcctccccctgccccccaggcctggggggccccccagggtccagtatgg 174

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Db 235 ctggtttcggatgggagcaagctgctccaggagactgactctgggctagggcata 294  
Qy 361 ACTGGTCTGCTGCCAGGACAGACACTGATGAGGACCTTACATCTGCCAGACCCCTGGA 420  
Db 295 actggtcttggccagcagacactga cyagggccctcacatctgcagagacctgga 354  
Qy 421 TGGTGCACTGGGGGCACAGTGCACCTGACCTGGCTGACCTCCAGCCGCCCTGTGT 480  
Db 355 tggctgacttggggcacagtgacctgcagctggctacctccagccgcctgtgt 414  
Qy 481 CTCCTGCCAACGACCGACTATGAGAACTTCTTGTGCACTTGGAGTCCACCGACATCAG 540  
Db 415 ctcttgcaagcagcgcactatgaaacttcttgcacttggagtcaccagccagatcag 474  
Qy 541 CGGTTTACCCACCCGCTACCTCCTACAGGAAGACAGCTCCTAGAGCTGATAG 600  
Db 475 cggtttaccacccgcgtacctccacctcctacaggaagacagtccttagagctgatg 534  
Qy 601 CCAGAGGAGGAGTCCATCCACAGGCGCCTGGCCATGCCACAGGATCCCTTAGGGGCTGC 660  
Db 535 ccagaggagagtgccatccacagggccctgcccagatcccttaggggctgc 594  
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RESULT 14  
AAA35197 standard; DNA; 1696 BP.  
XX AAA35197;  
XX 28-JUL-2000 (first entry)  
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:71.  
DE Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX Homo sapiens.  
OS  
XX WO200009525-A2.  
PN  
XX 24-FEB-2000.  
PD  
XX 03-AUG-1999; 99WO-US17712.  
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PR  
XX (UYEC-) UNIV EAST CAROLINA.  
PA  
XX Nyce JW;  
PI  
XX WPI; 2000-205971/18.  
DR  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers  
XX  
PS Disclosure; Page 1240; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,







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QY 1406 CAGGAGGCTTCGGCAGATTCCACCTATAATCCTGCTGCTGGTGGATAGAAACCCAG 1465
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Job time: 2726 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	857.6	47.6	897	106	AL562475	AL562475 AL562475
C 2	757.6	42.1	846	105	AL525319	AL525319 AL525319
C 3	687.8	38.2	833	147	BF339055	BF339055 602034848
C 4	664.8	36.9	722	106	AL580490	AL580490 AL580490
C 5	634.2	35.2	662	102	AL857919	AL857919 wj68b07.x
C 6	600.6	33.4	640	112	AL189494	AL189494 xt07d10.x
C 7	573.6	31.9	611	116	AW438628	AW438628 xt01c12.x
C 8	563.2	31.3	568	148	BF435972	BF435972 nab75h05.
C 9	547	30.4	547	148	BF434373	BF434373 7096c07.x
C 10	540	30.0	559	18	AL264000	AL264000 qi05b01.x
C 11	496.8	27.6	514	148	BF434707	BF434707 7p03d01.x
C 12	494.2	27.5	502	7	AA454657	AA454657 zx99g01.s
C 13	492.6	27.4	499	16	AL149448	AL149448 qc72h11.x
C 14	488	27.1	1067	155	BG537915	BG537915 602565788
C 15	474.4	26.4	528	7	AA456272	AA456272 zx99g01.r
C 16	474	26.3	556	110	AW008322	AW008322 wp53d07.x
C 17	472.8	26.3	782	144	BF100136	BF100136 601752311
C 18	472.2	26.2	527	165	BE261622	BE261622 601149311
C 19	467	25.9	539	116	AW440367	AW440367 xt14d07.x
C 20	460.2	25.6	466	16	AL095122	AL095122 qa19b09.x
C 21	457.4	25.4	474	165	BE262666	BE262666 601151083
C 22	456.4	25.4	578	31	AV605443	AV605443 AV605443
C 23	454	25.2	941	175	BG245059	BG245059 602357241
C 24	450.6	25.0	489	8	AA495792	AA495792 zw05a09.s
C 25	447.4	24.9	578	31	AV593468	AV593468 AV593468
C 26	447	24.8	1098	174	BG175402	BG175402 602337757
C 27	442.2	24.6	982	150	BF582653	BF582653 602094044
C 28	439	24.4	460	10	AA683522	AA683522 zf34c01.s
C 29	432.4	24.0	652	144	BF121766	BF121766 601755283
C 30	431.4	24.0	713	174	BG142647	BG142647 ia87f02.y
C 31	430	23.9	541	139	BE750928	BE750928 202602 MA
C 32	427.2	23.7	645	166	BE376991	BE376991 601227169
C 33	423.2	23.5	434	138	BE677751	BE677751 7f59g03.x
C 34	422.4	23.5	542	121	AW837043	AW837043 QV1-LN003
C 35	421.6	23.4	790	175	BG242042	BG242042 602354779
C 36	421	23.4	835	3	AA203740	AA203740 zx53c05.r
C 37	420.4	23.4	502	136	BE484826	BE484826 171613 BA
C 38	419.6	23.3	604	141	BE913237	BE913237 601668236
C 39	417.2	23.2	704	136	BE531796	BE531796 601230925
C 40	413.2	23.0	446	8	AA495728	AA495728 zw04a09.r
C 41	412.6	22.9	515	10	AA648383	AA648383 ns21e01.s
C 42	411.8	22.9	415	17	AI243648	AI243648 qn88c06.x
C 43	398.2	22.1	541	140	BE808981	BE808981 214306 MA
C 44	398	22.1	641	165	BE289392	BE289392 601089380
C 45	397.8	22.1	401	118	AW592445	AW592445 hf42f09.x

ALIGNMENTS

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LOCUS	AL562475	LTI_NFL003_NBC3	Homo sapiens	cdna clone	CS0DC011YP14 3
DEFINITION	prime, mRNA sequence.				
ACCESSION	AL562475				
VERSION	AL562475.1	GI:12910931			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W. B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope				

Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	Location/Qualifiers 1. .897 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DC011YP14" /clone.lib="LTI_NFL003_NBC3" /sex="male" /tissue.type="neuroblastoma cells" /lab_host="DH10B" /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"	BASE COUNT 212 a 276 g 167 t 3 others	Query Match 47.6%; Score 857.6; DB 106; Length 897; Best Local Similarity 99.0%; Pred. No. 8.6e-208; Indels 2; Gaps 2; Matches 882; Conservative 1; Mismatches 6;	QY 850 GACATACCTGCTCTGGCCGCTGGCAGCCGCCCTCTCTGCTCAAGTTCGCTTTGTCAGTA 909       DB 890 GACATACCTGCTCTGGCCGCTGGCAGCCGCCCTCTCTGCTCAAGTTCGCTTTGTCAGTA 832 QY 910 CGCTCGGCGCAGCATCCAGCTGCTCCAGCGTGGAGCCAGCTGGAGTGGAGAGGTAT 969       DB 831 CGCTCGGCGCAGCATCCAGCTGCTCCAGCGTGGAGCCAGCTGGAGTGGAGAGGTAT 772 QY 970 CACAGATGCTGTGGCTGGGCTG-CGCCATGCTGTACGAGTCAGTCCCGGAGCTTTCTAG 1028       DB 771 CACAGATGCTGTGGCTGGGCTGCCCATGCTGTACGAGTCAGTCCCGGAGCTTTCTAG 712 QY 1029 ATGCTGGCACCTGGAGCACCTGGAGCCCGGAGCCCTGGGAACTCCGAGACCTGGGACCA 1088       DB 711 ATGCTGGCACCTGGAGCACCTGGAGCCCGGAGCCCTGGGAACTCCGAGACCTGGGACCA 652 QY 1089 TACCAAGAGGATACACAGATGGGGCCAGCTACACAGCCAGCCAGAGGTGGAGCCCTCAGG 1148       DB 651 TACCAAGAGGATACACAGATGGGGCCAGCTACACAGCCAGCCAGAGGTGGAGCCCTCAGG 592 QY 1149 TGGACAGCCCTGCTCTCCAAAGCCCTCCCTCCCAACCCACACACCTCGGCTACTTTGATCACA 1208       DB 591 TGGACAGCCCTGCTCTCCAAAGCCCTCCCTCCCAACCCACACACCTCGGCTACTTTGATCACA 532 QY 1209 GGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTTGGGAATCCTTTCTTTCTGGGAC 1268       DB 531 GGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTTGGGAATCCTTTCTTTCTGGGAC 472 QY 1269 TGGTGGCTGGGGCCCTGGCACTGGGCTCTGGCTGAGGCTGACAGCGGTGGGAAGGATG 1328       DB 471 TGGTGGCTGGGGCCCTGGCACTGGGCTCTGGCTGAGGCTGAGACGGGGTGGGAAGGATG 412 QY 1329 GATCCCCAAAGCCCTGGGTTCTTGGCCCTCAGTGATTCAGTGGAGACGGCGTCCAGGAGCTC 1388       DB 411 GATCCCCAAAGCCCTGGGTTCTTGGCCCTCAGTGATTCAGTGGAGACGGCGTCCAGGAGCTC 352 QY 1389 CAAACCTGTAGAGACCCAGAGGGCTTGGCAGATTCACCTATATATCTGTCTTGTCTG 1448       DB 351 CAAACCTGTAGAGACCCAGAGGGCTTGGCAGATTCACCTATATATCTGTCTTGTCTG 292 QY 1449 GTGTGATAGAAACCAGGACAGACAGTAGATCCCTATGTTGGATCTCAGCTGGAAGTTC 1508       DB 291 GTGTGATAGAAACCAGGACAGACAGTAGATCCCTATGTTGGATCTCAGCTGGAAGTTC 232
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/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 194 a 181 c 265 g 193 t  
ORIGIN  
Query Match 38.2%; Score 687.8; DB 147; Length 833;  
Best Local Similarity 98.1%; Pred. No. 1.6e-164;  
Matches 717; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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QY 1065 GGGGAATCCGACACTGGGACCATACCAAGGAGATACACGATGGGGCCAGCTACACA 1124
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Db 1 GGGGAATCCGACACTGGGACCATACCAAGGAGATACACGATGGGGCCAGCTACACA 60
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QY 1125 CGCAGCCAGAGGTGGAGCCTCAGGTGGACAGCCTGCTCTCCAGGCGCCTCCCTCCCAAC 1184
|||||
Db 61 CGCAGCCAGAGGTGGAGCCTCAGGTGGACAGCCTGCTCTCCAGGCGCCTCCCTCCCAAC 120
|||||
QY 1185 CACACCTCGGCTACTTGATCACAGGACACTGTGTGGAGCAGGTAGCTGTGTCGCGCTT 1244
|||||
Db 121 CACACCTCGGCTACTTGATCACAGGACACTGTGTGGAGCAGGTAGCTGTGTCGCGCTT 180
|||||
QY 1245 TGGGAATCCTTTCTTCTGGGACTGTGTGGGCGGCTGGGACTGGGCTGTGGCTGA 1304
|||||
Db 181 TGGGAATCCTTTCTTCTGGGACTGTGTGGGCGGCTGGGACTGGGCTGTGGCTGA 240
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QY 1305 GGCTGAGACGGGTGGGAAGGTGGATCCCAAGCCTGGGTCTTCTGGCCTCAGTGATTC 1364
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Db 241 GGCTGAGACGGGTGGGAAGGTGGATCCCAAGCCTGGGTCTTCTGGCCTCAGTGATTC 300
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QY 1365 CAGTGGACAGCGTCCAGGAGCTCCAAACCTGTAGAGGACCCAGGAGGCTTGGCGAGAT 1424
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QY 1425 TCACCTATATCTGTCTGTGGTGTGGATAGAACAGGACAGGACAGTAGATCCCTA 1484
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Db 361 TCACCTATATCTGTCTGTGGTGTGGATAGAACAGGACAGGACAGTAGATCCCTA 420
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QY 1485 TGTTGGATCTCAGCTGGAAGTCTGTTTGGAGGCCATTTCTGTGAGACCTGTGATTTCA 1544
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Db 421 TGTTGGATCTCAGCTGGAAGTCTGTTTGGAGGCCATTTCTGTGAGACCTGTGATTTCA 480
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QY 1545 AATTGGCAGTGAAAGTGCTGTGTACCTGTGATTTACCCAGAGTGGAGTTCGTGTCA 1604
|||||
Db 481 AATTGGCAGTGAAAGTGCTGTGTACCTGTGATTTACCCAGAGTGGAGTTCGTGTCA 540
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QY 1605 AGGAACCTGTGATGTATGTATCTGTGTCCATGTGTGACCATGTGTGTGGAAGCAGGG 1664
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QY 1665 AACATGATTTCTCTGCAATCATGTATGTAGTGCTGGGAGTGTGTGGTCTCTTTGGC 1724
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Db 601 AACATGATTTCTCTGCAATCATGTATGTAGTGCTGGGAGTGTGTGGTCTCTTTGGC 660
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QY 1725 TCTTGGCCTTTCCCTTTCAGGGGTTGTGACGTGTGGAATAAGAGAATAAGGAAGTCT 1784
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QY 1785 TGGAGATATTA 1795
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Db 719 GGGACAAAAA 729

RESULT 4  
AL580490/c

LOCUS AL580490 LTI\_NFL008\_TC2 Homo sapiens cDNA clone CS0DJ015YH07 3  
DEFINITION prime, mRNA sequence.

ACCESSION AL580490  
VERSION AL580490.1 GI:12946563

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..722

source

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DJ015YH07"

/clone\_lib="LTI\_NFL008\_TC2"

/sex="male"

/tissue\_type="T cells from T cell leukemia"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA  
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enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 171 a 223 c 170 g 142 t 16 others

ORIGIN

Query Match 36.9%; Score 664.8; DB 106; Length 722;  
Best Local Similarity 95.0%; Pred. No. 1.1e-158;  
Matches 686; Conservative 14; Mismatches 10; Indels 12; Gaps 1;

QY 1012 TGCCCGGAGCTTTCTAGATGCTGGCACCTGGAGCACCTGGAGCCCGGAGGCTGGGGAA 1071

Db 722 TSCCCGGAGCTTTCTAGATGCTGGCACCTGGAGCACCTGGAGCCCGGAGGCTGGGGAA 663

QY 1072 TCCGAGCAGCTGGGACCATACCAAGGAGATACACGATGGGCGCAGCTACACAGCAGCC 1131

Db 662 TCCGAGCAGCTGGGACCATACCAAGGAGATACACGATGGGCGCAGCTACACAGCAGCC 603

QY 1132 AGAGGTGGAGCTCAGGTGGAGACGCCCTGCTCCCAAGGCCCTCCCTCCCAACACACCC 1191

Db 602 AGAGGTGGAGCTCAGGTGGAGACGCCCTGCTCCCAAGGCCCTCCCTCCCAACACACCC 543

QY 1192 TCGGCTACTTGATCACAGGAGCTCTGTGGAGCAGTAGCTGTGCTGGCGCTTTTGGGAAT 1251

Db 542 TCGGCTACTTGATCACAGGAGCTCTGTGGAGCAGTAGCTGTGCTGGCGCTTTTGGGAAT 483

QY 1252 CCTTTCTTCTCGGAGCTGGTGGCGCCTGGGCGCCTGGGCTCTGGCTGAGGCTGAG 1311

Db 482 CCTTTCTTCTCGGAGCTGGTGGCGCCTGGGCGCCTGGGCTCTGGCTGAGGCTGAG 423

QY 1312 ACGGGTGGGAGAGTGGATCCCAAGCCCTGGGCTTCTTGGCCCTCAGTGATTCAGTGGA 1371

Db 422 ACGGGTGGGAGAGTGGATCCCAAGCCCTGGGCTTCTTGGCCCTCAGTGATTCAGTGGA 363



SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 640)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Prepared by: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbrrp/image/image.html  
Seq primer: -400P from Gibco  
High quality sequence stop: 414.  
Location/Qualifiers  
1. .640  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2675539"  
/clone\_lib="NCI\_CGAP\_Ut4"  
/tissue\_type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: Sali;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo df.  
Average insert size 1.48 kb. Life Technologies catalog #:  
11542-016"  
BASE COUNT 180 a 192 c 136 g 132 t  
ORIGIN  
Query Match 33.4%; Score 600.6; DB 112; Length 640;  
Best Local Similarity 96.2%; Pred. No. 2.5e-142;  
Matches 615; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
QY 1157 CCTGCTCTCCAAAGGCCCTCCCTCCAAACACACCCCTGGCTACTGTATCATCAGGGACTCT 1216  
Db 640 CCGTGTCTTCAAAGCCCTCTTCCAAACACACCCCTGGCTACTGTATCCAAAGGACTCT 581  
QY 1217 GTGAGCAGTACTGTCTGGCGCTCTTTGGGAATCCTTTCTTCTGGGACTGGTGCT 1276  
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QY 1277 GGGCCCTGCACTGGGGCTCTGGCTGAGGCTGAGAGGGGGTGGAGGATGGATCCCCA 1336  
Db 520 GGGCCCTGCACTGGGGTCTGGCTGAGGCTGAGAGGGGGTGGAGGATGGATCCCCA 461  
QY 1337 AAGCCTGGGTCTTGGGCTCAGTGATTCACAGCAGGCGTCCAGGAGCTCCAAACCTG 1396  
Db 460 AAGCCTGGGTCTTGGGCTCAGTGATTCACAGCAGGCGTCCAGGAGCTCCAAACCTG 401  
QY 1397 TAGAGGACCCAGGAGGCTTCGGCAGATCCACCTATATATCTGTCTGTGTGGAT 1456  
Db 400 TAGAGGACCCAGGAGGCTTCGGCAGATCCACCTATATATCTGTGTGTGGAT 341  
QY 1457 AGAACCAGCAGCAGTAGATCCCTATGTTGGATCTCAGCTGGAAGTCTGTTTGA 1516  
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QY 1517 GCCATTCTGTGAGACCCCTGTATTTCAAATTTGCAGCTGAAAGGTCTGTACCTCTGA 1576  
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QY 1577 TTTCACCCAGAGTTGAGTTCTGCTCAAGAGAGGTGTGTAATGTGTACATCTGTGTCCA 1636  
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QY 1637 TGTGTGACCATGTGTCTGTGAAGCAGGGAACATGTATTCTCTGTCATCATGTATGTAGT 1696  
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QY 1697 GCTGGGGAGTGTGTGTGGCTCTTGGCTCTTGGCTTTCCCTTTCAGGGGTTGTGCAG 1756  
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QY 1757 GTGTGATTAAGAGTAAGGAAGTCTTCTGGAGATTATA 1795  
Db 40 GTGTGATAAAGAGAATAAGGAAGTCTTCTGGAGAAAAA 2  
RESULT 7  
AW438628/c  
LOCUS  
DEFINITION  
AW438628 611 bp mRNA EST 14-FEB-2000  
similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ; mRNA  
sequence.  
ACCESSION AW438628.1 GI:6973934  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 611)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Prepared by: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbrrp/image/image.html  
Seq primer: -400P from Gibco  
High quality sequence stop: 391.  
Location/Qualifiers  
1. .611  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:277878"  
/clone\_lib="NCI\_CGAP\_Ut4"  
/tissue\_type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: Sali;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo df.  
Average insert size 1.48 kb. Life Technologies catalog #:  
11542-016"  
BASE COUNT 172 a 195 c 124 g 120 t  
ORIGIN  
Query Match 31.9%; Score 573.6; DB 116; Length 611;  
Best Local Similarity 98.2%; Pred. No. 1.9e-135;  
Matches 601; Conservative 0; Mismatches 9; Indels 2; Gaps 2;  
QY 1190 CCTCGGCTACTTATCATCAGGAGTCTGTGGAGCAGGTAGCTGTGCTGGCTCTTTGGGA 1249  
Db 611 CCTGGGCTTATCATCAGGAGTCTGTGGAGCAGGTAGCTGTGCTGGCTCTTTGGGA 552  
QY 1250 ATCCTTTCTTTTCTTCTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1308  
Db 551 ATCCTTTCTTTTCTTCTTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 492





Db 132 CAGCGAGTCCGTGAAGCTGTGTTCTCTGGAGTGACTGCCGGGACCCAGTGTCTCTGGT 191  
Qy 306 TTCGGATGGGAGCAAGCTGCTCCAGGAGCTGACTCTGGGCTAGGCGATGAACATGG 365  
Db 192 TTCGGATGGGAGCAAGCTGCTCCAGGAGCTGACTCTGGGCTAGGCGATGAACATGG 251  
Qy 366 TCCTGGCCAGGCACAGCAGCTGATGAGGACACCTACATCTGCCAGACCCCTGGATGGT 425  
Db 252 TCCTGGCCAGGCACAGCAGCTGATGAGGACACCTACATCTGCCAGACCCCTGGATGGT 311  
Qy 426 CACTTGGGGGACAGTACCCTGGAGCTGGGCTACCTCCAGCCGCGCTGTGTCTCT 485  
Db 312 CACTTGGGGGACAGTACCCTGGAGCTGGGCTACCTCCAGCCGCGCTGTGTCTCT 371  
Qy 486 GCAAGCAGCCGACTATGAGAACTTCTCTTGACATTTGAGTCCAGCCAGATCAGCGGT 545  
Db 372 GCCAAGCAGCCGACTATGAGAACTTCTCTTGACATTTGAGTCCAGCCAGATCAGCGGT 431  
Qy 546 TACCCAGCCGCTACCTACCTCTACAGAGAGACAGTCTTAGAGCTGATGCCAGA 605  
Db 432 TACCCAGCCGCTACCTACCTCTACAGAGAGACAGTCTTAGAGCTGATGCCAGA 491  
Qy 606 GGAGAGTCCATCCACAGGCGCTGGCATGCCACAGATCCCTAGGGCTGCCGCT 665  
Db 492 GGAGAGTCCATCCACAGGCGCTGGCATGCCACAGATCCCTAGGGCTGCCGCT 551  
Qy 666 GTGTTGTC 673  
Db 552 GTGTTGTC 559

RESULT 11  
BF434707  
LOCUS BF434707 514 bp mRNA EST 29-NOV-2000  
DEFINITION 7p03d01.x1 NCI-CGAP\_Ov18 Homo sapiens cDNA clone IMAGE:3644593 3'  
similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ;, mRNA  
sequence.

ACCESSION BF434707  
VERSION BF434707.1 GI:11446995  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 514)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation; M. Bento  
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 341.  
Location/Qualifiers  
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/clone="IMAGE:3644593"  
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/tissue\_type="fibrotheloma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site:1: Not 1; Site:2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAGTGGGAGCGCGCGCCGACATTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 93 a 166 c 152 g 97 t  
ORIGIN

Query Match 27.6%; Score 496.8; DB 148; Length 514;  
Best Local Similarity 97.5%; Pred. No. 6.9e-116;  
Matches 501; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 109 ACTCTACCTCTCCCCACAGATGAGCAGAGCTGCTCAGGGCTGAGCAGGGTCTCTGTGTGC 168  
Db 1 ACTCTACCTCTCCCCACAGATGAGCAGAGCTGCTCAGGGCTGAGCAGGGTCTCTGTGTGC 60  
Qy 169 CGTGCTACAGCCCTGTGTCTCTCTCCCTCCCGCCAGGCTGGGGCCCCCAGG 228  
Db 61 CGTGCTACAGCCCTGTGTCTCTCTCCCTCCCGCCAGGCTGGGGCCCCCAGG 120  
Qy 229 GTTCCAGTATGGGACGAGCAGCTGCTGAAGCTGTCTCTCTCTGGAGTCACTGCCGG 288  
Db 121 GGTCCAGTATGGGACGAGCAGCTGCTGAAGCTGTCTCTCTCTGGAGTCACTGCCGG 180  
Qy 289 GGACCCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 348  
Db 181 GGACCCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Qy 349 GCTAGGGCATGAACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 408  
Db 241 GCTAGGGCATGAACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
Qy 409 CCAGACCTGGATGTGACCTTGGGGGACAGTCACTGACCTGACCTGACCTGACCTGACCTG 468  
Db 301 CCAGACCTGGATGTGACCTTGGGGGACAGTCACTGACCTGACCTGACCTGACCTGACCTG 360  
Qy 469 CGGCCCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 528  
Db 361 CGGCCCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
Qy 529 CAGCCAGATCAGCGGTGTACCCACCCGCTACCTCACTCTCTCTCTCTCTCTCTCTCTCTCT 588  
Db 421 CAGCCAGATCAGCGGTGTACCCACCCGCTACCTCACTCTCTCTCTCTCTCTCTCTCTCTCT 480  
Qy 589 AGGAGCTGATACGAGGAGGAGGAGTCCATCCACA 622  
Db 481 AGGAGCTGATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 514

RESULT 12  
AA454657/c  
LOCUS AA454657 502 bp mRNA EST 06-JUN-1997  
DEFINITION zx99g01.sl Soares\_NHMPu\_Sl Homo sapiens cDNA clone IMAGE:811920 3'  
similar to TR:G673438 G673438 CYTOKINE TYPE I RECEPTOR. ;, mRNA  
sequence.

ACCESSION AA454657  
VERSION AA454657.1 GI:2177433  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 502)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubouque, T., Geisel, G., Jost, S.,  
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,  
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,  
T., Waterston, R., and Willson, R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108



Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40m13 fwd. Et from Amersham  
High quality sequence stop: 443.

# .FEATURES

Location/Qualifiers

1. 502  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:811920"  
/clone\_lib="Soares\_NHMPu\_S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"

/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2N8HM, pregnant uterus NHMPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, and ss circles was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479." 2 others

BASE COUNT 138 a 157 c 102 g 103 t

## ORIGIN

Query Match 27.5%; Score 494.2; DB 7; Length 502;  
Best Local Similarity 99.0%; Pred. No. 3.1e-115;  
Matches 496; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1282 CTGGCACTGGGGCTCTGGCTGAGCGGTGGGAGGATGGATGCCCAAGCC 1341  
DB 502 CTGGCACTGGGGCTCTGGCTGAGCGGTGGGAGGATGGATGCCCAAGCC 443  
QY 1342 TGGGTTCTTGGCCTCAGTATCCAGTGCAGCGGCTCCAGGAGCTCCAAACCTGTAGAG 1401  
DB 442 TGGGTTCTTGGCCTCAGTATCCAGTGCAGCGGCTCCAGGAGCTCCAAACCTGTAGAG 383  
QY 1402 GACCCAGGAGGCTTCGGCAGATTCACCTATAATCTGTCTGTGGTGTGGATAGAA 1461  
DB 382 GACCCAGGAGGCTTCGGCAGATTCACCTATAATCTGTCTGTGGTGTGGATAGAA 323  
QY 1462 CCAGGAGGACAGTAGATCCCTATGTTGGATCTCAGCTGGAAGTCTCTGTTGGAGCCCA 1521  
DB 322 CCAGGAGGACAGTAGATCCCTATGTTGGATCTCAGCTGGAAGTCTCTGTTGGAGCCCA 263  
QY 1522 TTTCTGTGAGCCCTATTTCAAAATTCAGCTGAAAGGTGTTTACCTCTGATTTC 1581  
DB 262 TTTCTGTGAGCCCTATTTCAAAATTCAGCTGAAAGGTGTTTACCTCTGATTTC 203  
QY 1582 CCCAGAGTTGGAGTTCTGTCTCAAGAAAGCTGTGTAATGTGTACATCTGTGCCATGTGT 1641  
DB 202 CCCAGAGTTGGAGTTCTGTCTCAAGAAAGCTGTGTAATGTGTACATCTGTGCCATGTGT 143  
QY 1642 GACCATGTGTCTGGAAGCAGGAAATGATTAATCTCTGCATGATGATGATGAGTGCCTG 1701  
DB 142 GACCATGTGTCTGGAAGCAGGAAATGATTAATCTCTGCATGATGATGATGAGTGCCTG 83  
QY 1702 GGGAGTGTGTGGGCTTGGCTTTGGCTTTCCCTTTCAGGAGGTTGTGACAGTGTG 1761  
DB 82 GGGAGTGTGTGGGCTTGGCTTTGGCTTTCCCTTTCAGGAGGTTGTGACAGTGTG 23  
QY 1762 AATAAGAGAAATAGGAAGTT 1782  
DB 22 AATAAGAGAAATAGGAAGTT 2

## RESULT 13

AI149448/c

## LOCUS

DEFINITION

AI149448 499 bp mRNA EST 28-OCT-1998  
qc7h11.x1 Soares\_placenta\_8to9weeks\_2NBHP8to9W Homo sapiens CDNA  
clone IMAGE:1715205 3' similar to TR:064385 064385 INTERLEUKIN 11  
RECEPTOR, ALPHA CHAIN 2 PRECURSOR ; mRNA sequence.

## ACCESSION

AI149448

## VERSION

AI149448.1 GI:3677917

## KEYWORDS

EST.

## SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 499)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

This clone is available royalty-free through LLNL: contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert length: 1724 Std Error: 0.00

Seq primer: -40m13 fwd. Et from Amersham

High quality sequence stop: 459.

## FEATURES

Location/Qualifiers

1. 499

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1715205"

/dev\_stage="two placenta; one from 8 weeks and another

from 9 weeks post conception"

/lab\_host="DH10B (ampicillin resistant)"

/note="Organ: placenta; Vector: pT73D (Pharmacia) with a

modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGGATTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library constructed by Bento Soares and

M.Fatima Bonaldo."

BASE COUNT 141 a 154 c 99 g 105 t

## ORIGIN

Query Match 27.4%; Score 492.6; DB 16; Length 499;

Best Local Similarity 99.2%; Pred. No. 8e-115;

Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1295 CTCTGGCTGAGGCTGAGACGGGTGGAGGATGGATCCCAAGCCTGGTCTTGGCC 1354

DB 499 CTCTGGCTGAGGCTGAGACGGGTGGAGGATGGATCCCAAGCCTGGTCTTGGCC 440

QY 1355 TCAGTGATTCCAGTGGACAGCGCTCCAGGAGCTCCAAACCTGTAGAGAGCCAGAGGCG 1414

DB 439 TCAGTGATTCCAGTGGACAGCGCTCCAGGAGCTCCAAACCTGTAGAGAGCCAGAGGCG 380

QY 1415 TTGGGAGATTCCACCTATAATCTGTCTTGTGGTGTGGATAGAAACAGGAGGACAG 1474

DB 379 TTGGGAGATTCCACCTATAATCTGTCTTGTGGTGTGGATAGAAACAGGAGGACAG 320

QY 1475 TAGATCCCTATGTGTGATCTCAGCTGGAAGTTCTGTTTGGAGCCCAATTTCTGTGAGACC 1534

DB 319 TAGATCCCTATGTGTGATCTCAGCTGGAAGTTCTGTTTGGAGCCCAATTTCTGTGAGACC 260

QY 1535 CTGTAATTTCAAATTTGCAGCTGAAAGTGCTGTGTACCTCTGATTTCACCCAGAGTTGGA 1594

DB 259 CTGTAATTTCAAATTTGCAGCTGAAAGTGCTGTGTACCTCTGATTTCACCCAGAGTTGGA 200

QY 1595 GTTCTGCTCAAGGAAGCTGTGTAATGTGTACATCTGTGTCATCTGTGACCATGTGTCTG 1654



TITLE  
JOURNAL  
COMMENT

WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.lnlni.gov) for further information.  
Seq primer: -28ml3 rev2 Ef from Amersham  
High quality sequence stop: 504.

FEATURES

source

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/tissue\_type="Pooled human melanocyte, fetal heart, and  
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac  
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NbHPU, and fetal heart NbH19W) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."

BASE COUNT  
ORIGIN

98 a 176 c 157 g 97 t  
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Best Local Similarity 99.0%; Pred. No. 3.6e-110;  
Matches 519; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

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QY 794 CAGGGCCTCGGGTAGAGTACAGGTACCCGAGGCTGGAGCCAGCTGGACA 853  
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Db 68 CAGGGCCTCGGGTAGAGTACAGGTACCCGAGGCTGGAGCCAGCTGGACA 127  
QY 854 TACCCTGCTCTCTGCGCGTGGCCAGCCCACTTCCCTGCTCAAGTTCGTTTGCAGTACCGT 913  
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Db 128 TACCCTGCTCTCTGCGCGTGG-CAGGCCCACTTCCCTGCTCAAGTTCGTTTGCAGTACCGT 186  
QY 914 CCGGCGCAGCATCCAGCCTGTGTCCAGGTGGAGCCAGCTGGAGCTGGAGAGGTGATCACA 973  
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Db 187 CCGGCGCAG-ATCCAGCCTGTGTCCAGGTGGAGCCAGCTGGAGCTGGAGAGGTGATCACA 245  
QY 974 GATGCTGTGGCTGGGCTGCCCATGCTGTACGAGTCAGTGCCTGCCGGGACTTTCTAGATGCT 1033  
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Db 246 GATGCTGTGGCTGGGCTGCCCATGCTGTACGAGTCAGTGCCTGCCGGGACTTTCTAGATGCT 305  
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Db 306 GGCACCTGGAGCACCTGGAGCCGGA-GCTGGGAACTCCGAGCATCTGGGACCATACCA 364  
QY 1094 AAGGAGATACCATGGGGCCAGCTACACACGACCCAGAGGTGGAGCTCAGGTGGAC 1153  
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Db 365 AAGGAGATACCATGGGGCCAGCTACACACGACCCAGAGGTGGAGCTCAGGTGGAC 424  
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QY 1214 TCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCCTTTC 1257  
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Db 485 TCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCCTTTC 528

Search completed: October 3, 2001, 18:09:59  
Job time: 10334 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 3, 2001, 16:08:36 ; Search time 2420.96 Seconds  
(without alignments)  
11500.375 Million cell updates/sec

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Perfect score: 1800  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
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6: gb\_in3:\*  
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10: gb\_pat2:\*  
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12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_bal:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_higo\_hum:\*  
20: em\_higo\_inv:\*  
21: em\_higo\_rod:\*  
22: em\_hig\_hum1:\*  
23: em\_hig\_hum2:\*  
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25: em\_hig\_hum4:\*  
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29: em\_hig\_hum8:\*  
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96: gb\_in4:\*  
97: gb\_pr10:\*  
98: em\_ba3:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1643	91.3	1783	91	BC003110
2	1638.6	91.0	1682	93	HSIL11RM
3	1549.2	86.1	1696	97	HSU32324
4	1149.4	63.9	1199	93	HSIL11RR
5	982.6	54.6	1713	94	AF347936
6	975.4	54.2	1681	94	MMU14412
7	972	54.0	1719	94	MMETL
8	970.2	53.9	1985	94	MMILL1
					BC003110 Homo sapi
					Z38102 H.sapiens m
					U32324 Human inter
					Z46595 H.sapiens m
					AF347936 Rattus no
					U14412 Mus musculus
					X74953 M.musculus
					X98519 M.musculus





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Db 124 CAGGACGGTCCGTGAAGCTGTGTTGCTCTGGAGTGACTGCGGGGACCCAGCTGTCTCGGT 183
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Qy 366 TCCTGGCCAGGCACAGACACTGATGAGGGACCTACATCTGCCAGACCTCGATGGTG 425
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Qy 486 GCCAAGCAGCCGACTATGAGAACTTCTCTTGACATTTGGAGTCCAGCCAGATCAGCGGT 545
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Qy 606 GGAGGAGTCCATCCACAGGCGCTGCGCATGCCACAGATCCCTAGGGCTGCCCGCT 665
Db 484 GGAGGAGTCCATCCACAGGCGCTGCGCATGCCACAGATCCCTAGGGCTGCCCGCT 543
Qy 666 GTGTTGTCACGGGCTGAGTCTTGAGCCAGTACCGGATTAAATGTGACTGAGGTGAACC 725
Db 544 GTGTTGTCACGGGCTGAGTCTTGAGCCAGTACCGGATTAAATGTGACTGAGGTGAACC 603
Qy 726 CACTGGGTGGTCCAGACACAGCCCTGCTGTGGATGTGAGCTTGACAGACATCTTGGCCCTG 785
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Qy 906 AGTACCTCGGCGCAGCATCCAGCTGTGTCACGGTGGAGCCAGCTGAGCTGGAGGAG 965
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Qy 966 TGATCACAGATGCTGTGCTGGGCTGCCCATGCTGTACGAGTCACTGCCCGGACTTTC 1025
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Qy 1026 TAGATGCTGGCACCTGGAGCACCTGGAGCCCGAGGCGCTGGGGAACCTCCGAGCACTGGGA 1085
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Db 1141 GACTGGTGGTGGGCGCTGCACTGGGCTCTGGCTGAGCTGAGACGGGTGGGAAGG 1200
Qy 1326 ATGGATCCCCAAGCCTGGGTCTTGGCTCAGTGATTCCAGTGGACAGCGGTCCAGGAG 1385
Db 1201 ATGGATCCCCAAGCCTGGGTCTTGGCTCAGTGATTCCAGTGGACAGCGGTCCAGGAG 1260
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polyA\_signal

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Db 1619 GGGTTGTGACGTTGTAATAAGAGAATAAGGAAGTCTTGGAGATTACTCTAG 1673
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## RESULT 3

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HSU32324
LOCUS HSU32324 1696 bp mRNA PRI 22-NOV-1996
DEFINITION Human interleukin-11 receptor alpha chain mRNA, complete cds.
ACCESSION U32324
VERSION U32324.1 GI:975336
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1696)
AUTHORS Van Leuven, F., Stas, L., Hilliker, C., Miyake, Y., Billinski, P. and Gossler, A.
TITLE Molecular cloning and characterization of the human interleukin-11 receptor alpha-chain gene, IL11RA, located on chromosome 9p13
JOURNAL Genomics 31 (1), 65-70 (1996)
MEDLINE 96404003
REFERENCE 2 (bases 1 to 1696)
AUTHORS Van Leuven, F.
DIRECT SUBMISSION
TITLE Submitted (26-JUL-1995) Human Genetics, K.U.Leuven, Campus
JOURNAL Gasthuisberg ON06, Leuven, Belgium, B-3000
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## FEATURES

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## CDS



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Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 18; Indels 11;

5

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Db	55	CACCGAGATGAGCAGCAGCTGCTCAGGGCTGAGCAGGGTCTTGGTGGCCGTGGCTACAGC	114
Qy	181	CCTGGTCTGCTGCTCCTCCCTGCCCCCAGGGCTGGGGCCCCCAGGGTCCAGTATGG	240
Db	115	CCTGGTGTGCTGCTCCTCCCTGCCCCCAGGGCTGGGGCCCCCAGGGTCCAGTATGG	174
Qy	241	GCAGCCAGGAGGTCCTGTAAGCTGTGTTCTCTGGAGTGACTGCCGGGGACCCAGTGTG	300
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Qy	301	CTGTTTTCGGGATGGGGAGCCAAAGCTGTCACAGGACCTGACTCTGGGCTAGGGCATGA	360
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Qy	361	ACTGGTCTGCGCCAGGCACAGCAGCTGATGAGGGACCTACATCTGCCAGACCTCTGA	420
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Qy	421	TGGTGCACTTTGGGGCACAGTGACCCCTGCACTGGGCTACCCCTCCAGCCCGCCCTGTTG	480
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Qy	541	CGGTTTACCCACCCGCTACCTCACCCTCCTACAGAAAGACAGTCTCTAGGAGCTCATAG	600
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Qy	601	CCAGAGGAGAGTCCATCCACAGGGCCCTGGCCATGCCACAGGATCCCTTAGGGGCTCG	660
Db	535	CCAGAGGAGAGTCCATCCACAGGGCCCTGGCCATGCCACAGGATCCCTTAGGGGCTCG	594
Qy	661	CCGCTGTGTTGTCCACGGGCTCAGTTCTGAGGCCAGTACCGGATTAATGTGACTCAGCT	720
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Qy	721	GAACCCACTGGGTGGTGCCAGCAGCCCTGCTGATGTGAGCTTGACAGAGATCTTTGG	780
Db	655	GAACCCACTG -- GGTGCCAGCACAGCCTGCTGGATGTGAGCTTGACAGATCTTTGG	711
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[illegible]

## RESULT 4

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DEFINITION	H.sapiens mRNA for interleukin 11 receptor isoform (incomplete).				
ACCESSION	Z46595				
VERSION	Z46595.1 GI:995655				
KEYWORDS	interleukin 11 receptor; isoform.				
SOURCE	human.				

SOURCE	ORGANISM	Homio sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Humanat.		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

REFERENCE  
1 (bases 1 to 1199)  
Cherel, M., Sorel, M., Dubois, S., Lebeau, B., Moreau, J., Jacques, Y.  
AUTHORS  
and Minvielle, S.

**TITLE**  
Molecular cloning of human interleukin-11 receptor and Minville, S.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 11)  
AUTHORS Cherel M.

AUTHORS	CHERET, M.
TITLE	Direct Submission

JOURNAL. Submitted (04-NOV-1994) Michel Cherel, Institut de Biologie, INSERM U 211, 9 Quai de Moncousu, Nantes, 44035, FRANCE

FEATURES  
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BASE COUNT 211 a 387 c 371 g 230 t
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Best Local Similarity 99.7%; Pred. No. 6.5e-286;
Matches 1163; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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QY 194 TCCTCCCTCCCTCCAGGCTGGGGCCCCCAGGGGTCCAGTATGGGAGCCAGGCAGG 253
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QY 254 TCCTGGAAGCTGTGTCTGAGTGTGCTGCGGGGACCCAGTGTCTGTTTCGGGAT 313
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QY 374 CAGGCAGACAGCAGTATGAGGCGCCTACATCTGCCAGACCCCTGGATGGTGCACCTGGG 433
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QY 734 GTGGCAGCAGCAGCTGCTGTGATGTGAGTGTGAGCAGATCTTGGCGCTGACCCACCC 793
DB 598 GTGGCAGCAGCAGCTGCTGTGATGTGAGTGTGAGCAGATCTTGGCGCTGACCCACCC 657

QY 794 CAGGCGCTCGGGTAGAGTACAGTACAGTTACCCCGAGGCGCTCGAGCCAGCTGGACA 853
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QY 854 TACCCTGCTCCTGGCGTGGCCAGCCCACTTCCCTGCTCAAGTTCCTGTCAGTACCGT 913
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QY 914 CCGGCGCAGCAGTCCAGCCTGTGTCACGGTGGAGCGAGCTGGAGTGGAGAGGTATCACA 973
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DB 1018 AGCCCTGCTCCTCCAAAGCGCTCCTCCCAACCCACACCTCCGCTACTTCATCAGAGGAC 1077
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RESULT 5
AF347936 1713 bp mRNA ROD 05-APR-2001
LOCUS Rattus norvegicus Interleukin 11 receptor alpha chain precursor,
DEFINITION mRNA, complete cds.
ACCESSION AF347936
VERSION AF347936.1 GI:13549074
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Li,R., Hartley,L. and Robb,L.
TITLE Expression of Interleukin-11 and Interleukin-11 receptor alpha
chain in the rat uterus in the peri-implantation period
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1713)
AUTHORS Robb,L. and Li,R.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-2001) Cancer and Haematology Division, The Walter
and Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Vic 3050, Australia
FEATURES
source
1. 1713
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BASE COUNT 324 a 473 c 548 g 368 t  
ORIGIN

Query Match 54.6%; Score 982.6; DB 94; Length 1713;  
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Matches 1283; Conservative 0; Mismatches 334; Indels 30; Gaps 7;

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QY	186	TGCTGCTCCTCCCTCCCTGCCAGCCCTGGGCGCCCGCCAGGGTCCACATATGGGCAGC	245
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QY	246	CAGCAGGTCCTGGAAGCTGTGTCTGAGTGTGCTGGAGTGTGCTGGGAGCCCACTGTCTCTGGT	305
DB	175	CTGCGAGCCCGTGATGCTGTGCTGCCCGGAGTGAATGCTGGGACTCCGGTCTCTCTGGT	234
QY	306	TTGCGGATGGGAGCCAAAGCTGCTCCAGGACCTGACTCTGGGCTAGGGCATGAACCTGG	365
DB	235	TTGCGGATGGGAGCTCAGGCTGCTCCAGGAGCTGACTCTGGACTAGGACACAGACTGG	294
QY	366	TCCTGGCCAGGACAGACACTGATGAGGACCTACATCTCCAGACCCCTGGATGGTG	425
DB	295	TCCTGGCCAGGAGGACCGCTGACAGGGCTACTACGCTGTGCGACCTGGATGGTG	354
QY	426	CACCTGGGGGACAGTACACCTGAGCTGGGCTACCTCCAGCCCGCCCTGTGTCTCTCT	485
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QY	486	GCCAGCAGCCGACTATGAACTTCTTTGCACTTTGGACTTCCAGTCCCGACGACAGCGGTT	545
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QY	546	TACCCACCCCTACCTACCTCTACAGGAGAGACAGTCTCTAGGAGCTGATAGCCAGA	605
DB	475	TGCCCCCGGCTACCTTCTCTACAGGAGAGACAGTCTCTAGGAGCTGATAGCCAGA	534
QY	606	GGAGGAGTCCATCCAGGCGCTTGGCCATGCCACAGGATCCCTAGGGGCTGCCGCT	665
DB	535	GGAGAGTCCGCTACCGGGCTTGGCCATGCCACAGGATCCCTAGGGGCTGCCGAT	594
QY	666	GTGTGTCCACGGGCTGAGTCTTGGAGCAGTACCGGATTAATGTGACTGAGGTGAACC	725
DB	595	GTGTGTCCACGGGCGAGAGTCTTGGAGTGAATACCGGATCAATGTGACTGAGGTGAACC	654
QY	726	CACCTGGGTGGTCCAGCAGCAGCTGCTGATGTGAGCTTGCAGAGCATCTTGGCGCTG	785
DB	655	CAGTCTTGGCGGCGACGCTGCTGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	711
QY	786	ACCCACCCAGGGCTCGGGGTAGAGTCACTACAGGTTACCCCGAGGCTCGAGCCCA	845
DB	712	ATCCACCCAGGGCTCGGGGTGAATCACTACCTGCTACCCAGAGCGCTGCATGCCA	771
QY	846	GCTGGACATACCTGCTCTCTGGCGGTGCCAGCCCACTTCTCTGCTCAAGTCCGTTTC	905
DB	772	GCTGGACATACCTGCTCTCTGGCGGTGCCAGCCCACTTCTCTGCTCAAGTCCGTTTC	831
QY	906	AGTACCTCGGGCGCAGCATCCAGCTGGTCCAGGTTGGAGGAGGCTGGAGTGGAGGAGG	965
DB	832	ATATCCCTCCAGCAGCATCCAGCTGGTCCAGGTTGGAGGAGGCTGGTGGAGGAGT	891
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QY	1026	TAGATGTGACACTGGAGACCTTGGAGCCCGGAGGCTTGGGAGACTCCGAGCACTGGGA	1085

DB	952	TGATGCTGCGACCTGAGGTGCTTGGAGCCCGAGAGGCTGGGTACTCTCTAGCACCGGTC	1011
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DB	1012	CCCTGGGGATGAGTACCTGATGGAGCGGGGACACGACAGAGCTAGAGGCACAG	1071
QY	1143	CTCAGGTGGACAGCCCTGCTCTCCAAAGGCCCTCCCTCCAAACACACCCCTCGGCTACTTG	1202
DB	1072	CTCAGGAGGACAGCCCGCTCTCCAAAGGCCCTCTCTTGCAGCCAGACCCCAAGGCCACTTG	1131
QY	1203	ATCAGAGGACTCTGTGGAGCAGTACTGCTGGGGTCTTGGGGTCTTGGGAATCTTCTTTTC	1262
DB	1132	ATCAGAGGACCCCTTGGAGCAAGTGGCTGTGTAGCACTCTGGAATCTTCTCTTTTC	1191
QY	1263	TGGGACTGTGGCTGGGGCTTGGCACTGGGCTCTGGCTGAGGCTGAGACGGGGTGGGA	1322
DB	1192	TTGGCTGGCTGTGGAGCCCTGGCTCTGGGGTCTGGCTGAGGCTGAGGCGGAGTGGGA	1251
QY	1323	AGGATGGATCCCAAGCCCTGGGTTCTTGGCCCTCAGTGTATCCAGTGTCCAGGCGTCCAG	1382
DB	1252	AGGAGCGGCTCAAAAGCCCTGGCTTCTTGGCACCAATGATCCAGGGGACAAAGCTTCCAG	1311
QY	1383	GAGCTCCAAACCTGTAGAGGACCCAGGAGGCTTCCGACAGTCCACCTATATATCTCTGC	1442
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QY	1443	TTGCTGTGTGGATAGA-----AACCAGGAGGACAGTAGATCCCTATGGTTGG	1491
DB	1372	AGACTGGGTGGTTAAATGGACAGGAGGAGGAGGAGGAGGATCCCTATGGATGG	1431
QY	1492	ATCTCAGCTGGAAGTCTGTTTGGAGCCCATTTCTGTGAGACCCCTGATTTTCAAAAT	1548
DB	1432	AGGT---CTCAGTTCGAAGTCTGGAGCACCTTTCTTTGACACCTGAACTCCAACTTGCT	1488
QY	1549	TGAGCTGAAAGTGTGTGTACCTGTATTTACCCCGAGTGGAGTCTTCTGCTCAAGGA	1608
DB	1489	GCCAGCTGTCTCTCTGGACCTCTGATCCGCTCTTGGAGTGGAGTCCGCTCGAGGA	1548
QY	1609	ACGTGTGTAATGTATACATCTGTCTCCATGTGTGACCATGTGTGTGAGAGGAGGAACA	1668
DB	1549	CGGTG-----TATCGAAGTCTGTCTCTGTGACTGTGTGTGTGTGTGGGAGAGCA	1603
QY	1669	TGATTTCTCTGCACTGATGTATGTGGTGGCTTGGGAGTGTGTGGGTCTTGGGTCTTT	1728
DB	1604	CG--TTCTCGTGTGTGTGTATAGATGATGAGAGTGTGTGTGTGTGTGTGGGCTTG	1661
QY	1729	GGCCTTTCCCTTGCAGGGGTTGTGCA	1755
DB	1662	GCTCTCTCTGGGAGCATGGAGCGTAA	1688

RESULT 6

MMU14412	1681 bp	mrna	ROD	28-NOV-1994
LOCUS	Mus musculus	interleukin-11	receptor alpha-chain	mRNA, complete cds.
DEFINITION				
ACCESSION	U14412			
VERSION	U14412.1	GI:576454		
KEYWORDS				
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
TITLE	1 (bases 1 to 1681)			
JOURNAL	Hilton, D.J., Hilton, A., Raicevic, A., Rakar, S., Harrison-Smith, M., Gough, N.M., Begley, C.G., Metcalf, D., Nicola, N.A. and Willson, T.A.			
MEDLINE	Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high affinity binding and signal transduction			
REFERENCE	EMBO J. 13, 4765-4775 (1994)			
AUTHORS	95045367			
TITLE	2 (bases 1 to 1681)			
	Hilton, D.J.			
	Direct Submission			

JOURNAL	Submitted (07-SEP-1994)	Douglas J. Hilton, The Walter and Eliza Hall Institute of Medical Research, Royal Parade, Parkville, Victoria 3050, Australia
FEATURES	Location/Qualifiers	
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BASE COUNT	336 a 537 g 360 t	
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QY	69 ACCAGGTCCTGTGTGGCGTGGCTACAGCCCTGGTGTCTTCTCCTCCCTGCCCCAA 128	
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QY	212 GCCTGGGGCCCCCAGGGGTCCAGTATGGGCAGCCAGGCAGGTCCGTGAAGCTGTGTGT 271	
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QY	189 CCGGAGTGAGTGCTGGGACTCCAGTGTCTGTGTTTCGGGATGGAGATTCAGAGCTGCTC 248	
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QY	392 GAGGGCACTACATCTGCCAGACCCCTGGATGGTGCACCTTGGGGGCACAGTGACCCCTGCAG 451	
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QY	572 AGGAAGAAGCAGTCCTAGGAGCTGATAGCCAGAGGAGGAGTCCATCCAGGGGCCCTGG 631	
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QY	489 AGGAAGAAGACGCTGCCAGGAGCTGAGAGTTCAGAGGAAAGTCCATCCACGGGCCCTTGG 548	
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QY	632 CCATGCCCCACAGGATCCCTAGGGGCTGCCCGCTGTGTGTGTCACCGGGGCTTGACTTCTGG 691	
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QY	549 CCGTGTCCACAGGACCCTCTGGAGGCTCCCGATGTGTGGTCCATGGGCGAGACTTCTGG 608	
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QY	1024	TCATGATGCTGGACACCTGGAGCACCTGGAGCCCGGAGGCGCTGGGAACCTCCGAGCAGCTGG	1083
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QY	1138	GGAGGCTCAGGTGGAGACGCGCTGCTCCCAAGGCGCTCCCTCCCAACACACACCTCGGCT	1197
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QY	1258	TTTCTGGGACTGTTGGCTGGGGCCCTGGCACTGGGGCTCTGGCTGAGGCTGAGAGGGG	1317
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Db	1507	TGGGAAGGAGGACCGCAAAACCTGGGCTCTGGCACCCTGATCCCGTGGAAAGCT	1566
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Db	1964	GGAAAAAAA	1974
RESULT	9		
LOCUS	MMU69491		
DEFINITION	Mus musculus second IL11 receptor alpha chain (IL11R2) mRNA,	1975 bp	01-APR-1997
ACCESSION	U69491		
VERSION	U69491.1		
KEYWORDS	GI:1916003		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 1975)		
	Robb,L., Hilton,D.J., Willson,T.A. and Begley,C.G.		
	Structural analysis of the gene encoding the murine interleukin-11		
	receptor alpha-chain and a related locus		

J. Biol. Chem.	271 (23),	13754-13761	(1996)
6278810			
2	(bases 1 to 1975)		
Robb,L., Hilton,D.J., Brook-Carter,P.T. and Begley,C.G.			
Identification of a second murine interleukin-11 receptor			
alpha-chain gene (IL11R2) with a restricted pattern of expression			
Genomics	40 (3),	387-394	(1997)
97230451			
3	(bases 1 to 1975)		
Robb,L.			
Direct Submission			
Submitted (05-SEP-1996)	Walter and Eliza Hall Institute of Medical		
Research, Post Office, Royal Melbourne Hospital, Parkville,			
Victoria	3050, Australia		
Location/Qualifiers			
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QY	184	GGTGTCTCTCTCCCTGCCCGCAGGCTGGGGCCCCCAGGGGTCACAGTATGGGCA	243
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QY	244	GCCAGGAGTCCGTGAAGCTGTGTTGCTCGAGTACTGCCGGGACCCAGTGTCTTG	303
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QY	364	GGTCTGCGCCAGGACGACGACCTGATGAGGCGACCTACATCTCCAGACCTGGAT	423
Db	538	GGTCTGCGCCAGGTTGGACGCGCTGATGAAGCAGTATGCTGCCAGACCTGGAT	597
QY	424	TGCACTTGGGGGACAGTGACCTGACGCTGGGCTTACCTCCAGCCCGCTGTGTCT	483
Db	598	TGATATCAGGGGATGTTGACCTGAAGCTGGGCTTTCCCGCCAGCAGCTCTGAAG	657
QY	484	CTGCCAAGCAGCCGACTATGAGAACTTCTTGCATCTGGAGTCCCGCAGCATCAG	543
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838 ATGTGTGTTGTCAGGCGAGAGTTCTGGAGTGAGTACCGGATCAATGTGACCGAAGTGA 897
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Qy 1785 TGGAGATTATA 1795
Db 1111111111111111111111111111111111111111111111111111111
1952 GGAATAAAAAA 1962
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RESULT 10  
AX010400  
LOCUS AX010400 1140 bp DNA PAT 06-SEP-2000  
DEFINITION Sequence 3 from Patent WO9959608.  
ACCESSION AX010400  
VERSION AX010400.1 GI:9997251  
SOURCE Murinae gen. sp.  
ORGANISM Murinae gen. sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 1140)  
AUTHORS Austin, R.C. and Shaughnessy, S.  
TITLE Osteoporosis treatment  
PATENT: WO 9959608-A 3 25-NOV-1999;  
JOURNAL HAMILTON CIVIC HOSPITAL RESEAR (CA)  
FEATURES  
source 1. .1140  
terminator /organism="Murinae gen. sp."  
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BASE COUNT 223 a 344 c 347 g 226 t  
ORIGIN

Query Match 43.5%; Score 783.6; DB 9; Length 1140;  
Best Local Similarity 83.0%; Pred. No. 1.7e-191;  
Matches 920; Conservative 0; Mismatches 179; Indels 9; Gaps 2;

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Db 1 ATGAGCAGCAGCTCTCAGGCTGACCAGGCTCTGTGGCCGTGGCTACGCGCCCTGGT 60
Qy 188 TCTGCTCTCCCTCCCTGCCCCAGGCTGGGGCCCCAGGGTCCAGTATGGGCAGCCA 247
Db 1 TCTTCTCTCCCTCCCTGCCCCAAGCTTGGGTCTCCAGGGGTCCAGTATGGACAACCT 120
Qy 248 GGCAGGTCCGTGAAGCTGTGTTCCTGGAGTGACTGCCGGGGACCCAGTGTCTCTGTTT 307
Db 121 GCGAGGCCGTGATGCTGTGCTGCCCGGAGTGAGTGTGGGACTCCAGTGTCTCTGTTT 180
Qy 308 CGGATGGGAGCAAAAGCTCTCCAGGACCTCAGTCTGGCTAGGGCATGAAGTGGT 367
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Qy	548	CCACCCGCTACTC	ACCTCTTACAGG	AAGAAGACAGTCTCTAGGAGCTGTATGACCGAGG	607
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D <sub>b</sub>	421	CCACCCGCTACTCTTACTTCTTACAGG	AAGAAGACGCTGCCAGGAGCTGAGAGTCGACGAGG	480	
Qy	608	AGGAGTCCATCCACAGG	CGCCTGGCCATGCCACAGGATCCCTTAGGGGCTGCCCCTGT	667	
D <sub>b</sub>	481	GAAGTCCATCCACCGG	CGCTTGGCCGTGTCACAGGACCCCTCTGGAGGCTCTCCGATGT	540	
Qy	668	GTTGTCCACGGGGCTGAGTCTTGAG	CCCAAGTACC	CGGATTAATGTGACTGAGGTGAACCCA	727
D <sub>b</sub>	541	GTGTCATATGGGCGACAGTCTTGAG	TGAGTGAATACCGGATCAATGTGACCGAGGTGAACCCA	600	
Qy	728	CTGGTGTGTCAGACACACGCTGCTG	GATGTGACTTGCAGAGCATCTTCGCGCCCTGAC	787	
D <sub>b</sub>	601	CTG---	GGTGCCAGCAGTCCCTACTG	ATGTGAGTATACAGAGCATCTTCGCGTCTGAT	657
Qy	788	CCACCCAGGGCCTGCGGTAGAGTCA	GTACAGAGTTACCCCGGAGGCTCTCGAGCCAGC	847	
D <sub>b</sub>	658	CCACCCCAAGGACTGCGGGTGAAT	CCGTACCTAGTTACCCGAGAGCGCTGCATGCCAGC	717	
Qy	848	TGACATATCCCTGCCTCTGCGCGT	GCCAGCCGCACTTCTGCTCAAGTTCGGTTTCGAG	907	
D <sub>b</sub>	718	TGACATATCCCTGCCTCTGCGG	CTGCCAACCCCACTTCTGTCTCAAGTTCGGGTGCCA	777	
Qy	908	TACCGTCCGGCGGACGATCCAGC	CTGGTCCACGGTGGAGCCAGCTGGAGTCTGGAGGAGTG	967	
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D <sub>b</sub>	838	ATAACAGATGCTGTGCTGGGTG	CCACACGGGTACAGTCAAGTCAAGTGGC	CGGAGGATCTTCTG	897
Qy	1028	GATGCTGGACCTTGGAGCACCT	GGAGCCCGGAGGCTCGGGAACCTCCGAGCACTGGGACC	1087	
D <sub>b</sub>	898	GATGCTGGCACCTTGGAGCG	CTGGAGCCACAGAGGCTGGGTACTCTTAGCACTTGGTCCC	957	
Qy	1088	ATACCAAGGAGATACCA	GATGGGCGCAGCTACACACGACG	-----CAGAGGTGGAG	1141
D <sub>b</sub>	958	CTGCGAGATGAGATACCTGAT	TGGAGCCAGGACACGACAGCAGCTAGAGGCGAGTAGTA	1017	
Qy	1142	CCTCAGTGGACAGCCCTGCTC	CTCCAAGGCCCTCCCTTCCAACACACCCCTCGGCTACTT	1201	
D <sub>b</sub>	1018	GCTCAGGAGGACACCCGG	CTCCTGCAAGGCCCTTCTTGCAGCCGACCCCAAGGCCACTT	1077	
Qy	1202	GATCACAGGGACTCTCTG	TGGACAGGCTAG	1229	
D <sub>b</sub>	1078	GATCACAGGGATCCCTT	GGGAGCAACTGG	1105	

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RESULT 11
AL450283
LOCUS
DEFINITION
AL450283 176042 bp DNA HTG 19-MAR-2001
Homo sapiens chromosome 9 clone RP11-443P11, *** SEQUENCING IN
PROGRESS ***, 5 unordered pieces.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (16-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequests@sanger.ac.uk
On Mar 20, 2001 this sequence version replaced gi:13375015.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk

```

```

Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA443P11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 175329 bases at least Q40
Consensus quality: 175422 bases at least Q30
Consensus quality: 175505 bases at least Q20
Insert size: 175642; sum-of-contigs
Insert size: 152620; 6.2% error; agarose-fp
Quality coverage: 12.58x in Q20 bases; sum-of-contigs Quality
coverage: 14.57x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 7824: contig of 7824 bp in length
* 7825 7924: gap of 100 bp
* 7925 12465: contig of 4522 bp in length
* 12447 12546: gap of 100 bp
* 12347 15642: contig of 7096 bp in length
* 19643 19742: gap of 100 bp
* 19743 139602: contig of 119860 bp in length
* 139603 139702: gap of 100 bp
* 139703 176042: contig of 36340 bp in length

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FEATURES	SOURCE
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[illegible]

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ACCESSION AL162231  
VERSION AL162231.20 GI:13160220  
KEYWORDS HTG.  
SOURCE human.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1 (bases 1 to 186433)  
Clark, G.  
Direct Submission  
Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Feb 27, 2001 this sequence version replaced gi:12956907.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em', EMBL; Sw',  
SWISSPROT; Tr', TREMBL; Wp', WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C-elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr9  
RP11-195F19 is from the library RP11-195F19 constructed by the group  
of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBAC3.6  
This sequence is the entire insert of clone RP11-195F19 The true  
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FEATURES  
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Matches 439; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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RESULT 13  
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ACCESSION G26821  
VERSION G26821.1 GI:1349053  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE human STSs derived from sequences in dbEST and the Unigene  
collection.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 411)  
Hudson, T.  
Whitehead Institute/MIT Center for Genome Research; Physically  
Mapped STSs  
Unpublished (1995)  
JOURNAL  
COMMENT  
Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900

Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: GCAGCAGTAGATCCCTATGG  
Primer B: GCATGCAGACATACATGTTCC  
STS size: 219  
PCR Profile:

Presoak:  
Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primers: each 5 pM  
dNTPs: each 4 mM  
Taq Polymerase: 0.025 units/ul  
Total Vol: 20 ul

Buffer:  
MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 9.3

Derived from dbEST (genbank accession Z38102).

Location/Qualifiers

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BASE COUNT 95 a 76 c 118 g 122 t  
ORIGIN

Query Match 21.4%; Score 385.2; DB 54; Length 411;  
Best Local Similarity 98.8%; Pred. No. 1.4e-88;  
Matches, 399; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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Db 1 TAGAGACCCAGGAGGCTTCGGCAGATCCACCTAATCCCTGCTTGTGTTGGAT 60  
QY 1457 AGAAACCCAGGACGAGTAGATCCCTATGTTGGATCTCAGCTGGAAGTCTGTTTGA 1516  
Db 61 AGAAACCCAGGACGAGTAGATCCCTATGTTGGATCTCAGCTGGAAGTCTGTTTGA 120  
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Db 121 GCCATTTCTGTGAGACCTGTATTTCAATTTGCAGCTGAAGGTGCTGTACCTCTGA 180  
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Db 181 TTTCACCCAGAGTTGAGTTCTGCTCAAGAACGTTGTAAATGTTACATCTGTGTCCA 240  
QY 1637 TGTGTGACCATGTTCTGTGAAGCAGGGAACATGTAATCTCTGCATGCATGTATGAGT 1696  
Db 241 TGTGTGACCATGTTCTGTGAAGCAGGGAACATGTAATCTCTGCATGCATGTATGAGT 300  
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VERSION U32323.1 GI:975334  
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ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 9286)  
AUTHORS Van Leuven,F., Stas,D., Hilliker,C., Miyake,Y., Bilinski,P. and Gossler,A.  
TITLE Molecular cloning and characterization of the human interleukin-11 receptor alpha-chain gene, IL11RA, located on chromosome 9p13  
JOURNAL Genomics 31 (1), 65-70 (1996)  
MEDLINE 96404003  
REFERENCE 2 (bases 1 to 9286)  
AUTHORS Van Leuven,F.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-1995) Human Genetics, K.U.Leuven, Campus Gasthuisberg ON06, Leuven, Belgium, B-3000  
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